

Copyright GenCore version 5.1.6  
(c) 1993 - 2005 Compugen Ltd.

**OM protein - protein search, using sw model**

Run on: July 13, 2005, 09:25:40 ; Search time 94.5296 Seconds  
(without alignments)  
878.681 Million cell updates/sec

Title: US-09-819-371-6  
Perfect score: 215  
Sequence: 1 IAEVYDDTQPLRFDSAAI.....QRDGEETQDTTELVTRPAG 215

Scoring table: Oligo Gapext 60.0 , Gapext 60.0

Searched: 1726220 seqs, 386332138 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications\_AA:  
 1: /cggn2\_6\_ptodata/1/pubppa/US07\_PUBCOMB.pep:  
 2: /cggn2\_6\_ptodata/1/pubppa/PCT\_NEW\_PUB.pep:  
 3: /cggn2\_6\_ptodata/1/pubppa/US06\_NEV\_PUB.pep:  
 4: /cggn2\_6\_ptodata/1/pubppa/US06\_PUBCOMB.pep:  
 5: /cggn2\_6\_ptodata/1/pubppa/PCTUS\_PUBCOMB.pep:  
 6: /cggn2\_6\_ptodata/1/pubppa/US07\_NEV\_PUB.pep:  
 7: /cggn2\_6\_ptodata/1/pubppa/US08\_NEV\_PUB.pep:  
 8: /cggn2\_6\_ptodata/1/pubppa/US09\_PUBCOMB.pep:  
 9: /cggn2\_6\_ptodata/1/pubppa/US09A\_PUBCOMB.pep:  
 10: /cggn2\_6\_ptodata/1/pubppa/US09B\_PUBCOMB.pep:  
 11: /cggn2\_6\_ptodata/1/pubppa/US09C\_PUBCOMB.pep:  
 12: /cggn2\_6\_ptodata/1/pubppa/US09\_NEV\_PUB.pep:  
 13: /cggn2\_6\_ptodata/1/pubppa/US10A\_PUBCOMB.pep:  
 14: /cggn2\_6\_ptodata/1/pubppa/US10B\_PUBCOMB.pep:  
 15: /cggn2\_6\_ptodata/1/pubppa/US10C\_PUBCOMB.pep:  
 16: /cggn2\_6\_ptodata/1/pubppa/US10D\_PUBCOMB.pep:  
 17: /cggn2\_6\_ptodata/1/pubppa/US10E\_PUBCOMB.pep:  
 18: /cggn2\_6\_ptodata/1/pubppa/US10\_NEV\_PUB.pep:  
 19: /cggn2\_6\_ptodata/1/pubppa/US11A\_PUBCOMB.pep:  
 20: /cggn2\_6\_ptodata/1/pubppa/US11\_NEV\_PUB.pep:  
 21: /cggn2\_6\_ptodata/1/pubppa/US60\_NEV\_PUB.pep:  
 22: /cggn2\_6\_ptodata/1/pubppa/US60\_PUBCOMB.pep:

12 32 14.9 110 14 US-10-040-862-799  
13 32 14.9 110 14 US-10-040-862-2139  
14 32 14.9 110 15 US-10-057-4758-2139  
15 32 14.9 110 15 US-10-154-8848-799  
16 32 14.9 110 15 US-10-154-8848-2139  
17 32 14.9 110 16 US-10-764-324-799  
18 32 14.9 110 16 US-10-764-324-2139  
19 32 14.9 110 16 US-10-262-839-48  
20 32 14.9 110 15 US-10-264-049-3505  
21 32 14.9 110 15 US-10-028-049-3505  
22 32 14.9 110 15 US-10-741-600-941  
23 30 14.0 104 9 US-09-925-302-035  
24 30 14.0 104 9 US-09-923-302-835  
25 30 14.0 104 9 US-10-085-198-72  
26 30 14.0 371 15 US-10-210-172-156  
27 28 13.0 91 14 US-10-028-386-31089  
28 28 13.0 476 16 US-10-430-984-16  
29 28 13.0 500 16 US-10-430-984-15  
30 23 10.7 371 15 US-10-029-386-34273  
31 23 10.7 96 14 US-10-029-386-28377  
32 19 8.8 371 15 US-10-435-115-363890  
33 17 7.9 91 14 US-09-858-580-21  
34 17 7.9 184 9 US-09-858-580-21  
35 17 7.9 184 10 US-09-847-172-21  
36 17 7.9 421 15 US-10-941-152-21  
37 17 7.9 421 15 US-10-210-172-174  
38 16 7.4 91 9 US-09-864-761-38005  
39 16 7.4 92 15 US-10-380-880-5  
40 16 7.4 145 9 US-09-810-560-8  
41 16 7.4 198 16 US-10-741-601-387  
42 16 7.4 198 17 US-10-741-601-1143  
43 16 7.4 234 15 US-10-380-880-8  
44 16 7.4 251 16 US-10-741-601-384  
45 16 7.4 251 17 US-10-741-600-1142

## ALIGNMENTS

RESULT 1.  
US-09-19-371-6  
; Sequence 6, Application US/09819371  
; Publication No. US200400533441  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Ca  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO: 6  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-6

Query Match 100.0% Score 215; DB 11; Length 215;  
Best Local Similarity 100.0%; Pred. No. 6.4e-203;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IAVYYVDTQPLRFDSAAIPRMMPREPMWQEGPQTYWITCYAKANQTDYVALRNLL 60  
Db 1 IAVYYVDTQPLRFDSAAIPRMMPREPMWQEGPQTYWITCYAKANQTDYVALRNLL 60

Qy 61 RRYNQSEAGSHTLQGNGCDMGPDRGLRGTQHAWDKDYLISLNEDLRSWTAATDVAQI 120  
Db 61 RRYNQSEAGSHTLQGNGCDMGPDRGLRGTQHAWDKDYLISLNEDLRSWTAATDVAQI 120

Qy 121 TQRFYEAEEFRTYLEGECLELRYLENGKETLQRADPPKAHVAAHHPTSDHEATLR 180  
Db 121 TQRFYEAEEFRTYLEGECLELRYLENGKETLQRADPPKAHVAAHHPTSDHEATLR 180

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	215	100.0	215	11 US-09-819-371-6	Sequence 6, Appli
2	119	55.3	271	9 US-09-925-301-1431	Sequence 1431, Ap
3	119	55.3	274	11 US-09-819-371-5	Sequence 5, Appli
4	119	55.3	362	15 US-10-257-021-82	Sequence 82, Appli
5	119	55.3	442	16 US-10-408-765A-1887	Sequence 1887, Ap
6	95	44.2	362	11 US-09-819-371-4	Sequence 4, Appli
7	55	25.6	96	14 US-10-029-386-30718	Sequence 30718, A
8	52	24.2	186	15 US-10-264-049-4063	Sequence 4063, Ap
9	32	14.9	91	9 US-09-864-761-35461	Sequence 35461, A
10	32	14.9	110	9 US-09-796-692-799	Sequence 799, App
11	32	14.9	110	9 US-09-796-692-2139	Sequence 2139, Ap

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Qy 181 CWALGFYDPAEITLTWQRGEBOTQDTTELVETRPAG 215  
 Db 181 CWALGFYDPAEITLTWQRGEEOTQDTTELVETRPAG 215

**RESULT 2**  
 US-09-925-301-1431  
 ; Sequence 1431, Application US/09925301  
 ; Patent No. US20020052308A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA106  
 ; CURRENT APPLICATION NUMBER: US/09 925, 301  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124, 270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 1694  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1431  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-925-301-1431

Query Match 55.3%; Score 119; DB 9; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 2e-108;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 DGKDYSISNEDLRSWTAADTVQITORYEAEYAAEERTYDEGCECLLRRYLENGKET 156  
 Db 146 DGKDYSISNEDLRSWTAADTVQITORYEAEYAAEERTYDEGCECLLRRYLENGKET 205  
 Qy 157 LQRADPPKAHVAAHPISDHEATLRCWAALGFYPAAEITLTWQRDGEQTQDTTELVETRPAG 215  
 Db 206 LQRADPPKAHVAAHPISDHEATLRCWAALGFYPAAEITLTWQRDGEQTQDTTELVETRPAG 264

**RESULT 3**  
 US-09-819-371-5  
 ; Sequence 5, Application US/09919371  
 ; Publication No. US2004005344A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Egawa, Kohji  
 ; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can  
 ; FILE REFERENCE: 30815  
 ; CURRENT APPLICATION NUMBER: US/09/819, 371  
 ; CURRENT FILING DATE: 2002-03-15  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SEQ ID NO 5  
 ; LENGTH: 274  
 ; SOFTWARE: PatentIn version 3.0  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-819-371-5

Query Match 55.3%; Score 119; DB 11; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 2e-108;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 DGKDYSISNEDLRSWTAADTVQITORYEAEYAAEERTYDEGCECLLRRYLENGKET 156  
 Db 119 DGKDYSISNEDLRSWTAADTVQITORYEAEYAAEERTYDEGCECLLRRYLENGKET 178  
 Qy 157 LQRADPPKAHVAAHPISDHEATLRCWAALGFYPAAEITLTWQRDGEQTQDTTELVETRPAG 215  
 Db 179 LQRADPPKAHVAAHPISDHEATLRCWAALGFYPAAEITLTWQRDGEQTQDTTELVETRPAG 237

**RESULT 4**  
 US-10-257-021-82  
 ; Sequence 82, Application US/10257021  
 ; Publication No. US20030211498A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morin, Patrice J.  
 ; APPLICANT: Sherman-Baust, Cheryl A.  
 ; APPLICANT: Pizer, Ellen S.  
 ; APPLICANT: Hough, Colleen D.  
 ; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER  
 ; FILE REFERENCE: 14014\_0369U2  
 ; CURRENT APPLICATION NUMBER: US/10/257,021  
 ; CURRENT FILING DATE: 2002-10-03  
 ; PRIOR APPLICATION NUMBER: PCT/US01/10947  
 ; PRIOR FILING DATE: 2001-04-03  
 ; PRIOR APPLICATION NUMBER: 60/194,336  
 ; PRIOR FILING DATE: 2000-04-03  
 ; NUMBER OF SEQ ID NOS: 147  
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0  
 ; SEQ ID NO 82  
 ; LENGTH: 362  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-257-021-82

Query Match 55.3%; Score 119; DB 15; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 2.e-108;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 DGKDYSISNEDLRSWTAADTVQITORYEAEYAAEERTYDEGCECLLRRYLENGKET 156  
 Db 140 DGKDYSISNEDLRSWTAADTVQITORYEAEYAAEERTYDEGCECLLRRYLENGKET 199

**RESULT 5**  
 US-10-408-765A-1887  
 ; Sequence 1887, Application US/10408765A  
 ; Publication No. US20040101874A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Pany, Boin D.  
 ; APPLICANT: Zhang, Bing  
 ; APPLICANT: Gibson, Bradford W.  
 ; APPLICANT: Taylor, Steven W.  
 ; APPLICANT: Glenn, Gary M.  
 ; APPLICANT: Warnock, Dale E.  
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
 ; FILE REFERENCE: 660088 465  
 ; CURRENT APPLICATION NUMBER: US/10/408,765A  
 ; CURRENT FILING DATE: 2003-04-04  
 ; NUMBER OF SEQ ID NOS: 3077  
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0  
 ; SEQ ID NO 1887  
 ; LENGTH: 442  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-408-765A-1887

Query Match 55.3%; Score 119; DB 16; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 3.e-108;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 DGKDYSISNEDLRSWTAADTVQITORYEAEYAAEERTYDEGCECLLRRYLENGKET 156  
 Db 140 DGKDYSISNEDLRSWTAADTVQITORYEAEYAAEERTYDEGCECLLRRYLENGKET 199  
 Qy 157 LQRADPPKAHVAAHPISDHEATLRCWAALGFYPAAEITLTWQRDGEQTQDTTELVETRPAG 215

Db 200 LQRADPPKAHVAAHHPISDHEATLRCWALGFYPAEITLTWORDGEEQTDTELVTRPAG 258

Publication No. US20040005579A1

RESULT 6  
US-09-819-371-4  
Sequence 4, Application US/0919371  
Publication No. US20040053344A1  
GENERAL INFORMATION:  
APPLICANT: Egawa, Kohji  
TITLE OF INVENTION: Cancer Cell-Specific HLA-P Antigen and a Diagnostic Method of Cancer  
FILE REFERENCE: 30815  
CURRENT APPLICATION NUMBER: US/09/819,371  
CURRENT FILING DATE: 2002-03-15  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 4  
LENGTH: 362  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-819-371-4

Query Match 44.2%; Score 95; DB 11; Length 362;  
Best Local Similarity 100.0%; Pred. No. 1e-84;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IAEVYDTQFLRFDSDAAIPRMEEPRPWPVQEQQWMTGAKANAVQTDVRLNLL 60  
44 IAEVYDTQFLRFDSDAAIPRMEEPRPWPVQEQQWMTGAKANAVQTDVRLNLL 103

Qy 61 RRYNGSEAGSHTLQGMNGCDMGPDGRLLRGYHQHA 95  
Db 104 RRYNGSEAGSHTLQGMNGCDMGPDGRLLRGYHQHA 138

RESULT 7  
US-10-029-386-30718  
Sequence 30718, Application US/10029386  
Publication No. US20050194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENOTYPING  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: AEMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO: 30718  
LENGTH: 96  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR6 1  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12  
OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52  
US-10-029-386-30718

Query Match 25.6%; Score 55; DB 14; Length 96;  
Best Local Similarity 100.0%; Pred. No. 6.0e-46;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

161 DPPKAVAHHPISDHEATLRCWALGFYPAEITLTWORDGEEQTDTELVTRPAG 215  
2 DPPKAVAHHPISDHEATLRCWALGFYPAEITLTWORDGEEQTDTELVTRPAG 56

RESULT 8  
US-10-264-049-4063  
Sequence 4063, Application US/10264049

Query Match 24.2%; Score 52; DB 15; Length 186;  
Best Local Similarity 100.0%; Pred. No. 1.e-42;  
US-10-264-049-4063

**RESULT 9**

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 8  
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 11  
 OTHER INFORMATION: EST HUMAN HIT: AV820231.1, EVALU 3.00e-52  
 OTHER INFORMATION: SWISSPROT HIT: P30487, EVALU 3.00e-53  
 US-09-864-761-35461

Query Match 14.9%; Score 32; DB 9; Length 91;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-23;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 HHPISDHEATLRCWALGFYPAEITLTQRDGE 200  
 Db 8 HHPISDHEATLRCWALGFYPAEITLTQRDGE 39

RESULT 10

US-09-796-692-799

Sequence 799, Application US/09796692  
 Publication No. US20020198362A1

GENERAL INFORMATION

APPLICANT: Pean, Sharron G.  
 APPLICANT: Rank, David R.  
 APPLICANT: Hanzel, David K.  
 APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEAR ACID PROBES USEFUL FOR FILE REFERENCE: Aemlica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-16

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00656

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00657

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00654

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00659

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00655

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00658

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00653

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00651

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/668,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annotrax Sequence Listing Engine vers. 1.1

SEQ ID NO 35461

LENGTH: 91

TYPE: PER

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AP000507.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 24

OTHER INFORMATION: EXPRESSED IN HBL106, SIGNAL = 53

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 47

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 17

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 32

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 58

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 15

Query Match 14.9%; Score 32; DB 9; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-23;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 HHPISDHEATLRCWALGFYPAEITLTQRDGE 200  
 Db 67 HHPISDHEATLRCWALGFYPAEITLTQRDGE 98

RESULT 11

US-09-796-692-2139

Sequence 2139, Application US/09796692  
 Publication No. US20020198362A1

GENERAL INFORMATION:  
 APPLICANT: Gaiger, Alexander  
 APPLICANT: Algate, Paul A.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
 TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES  
 FILE REFERENCE: 2077\_001200  
 CURRENT APPLICATION NUMBER: US/09/796,692  
 CURRENT FILING DATE: 2001-03-01  
 PRIOR APPLICATION NUMBER: 60/186,126  
 PRIOR FILING DATE: 2000-03-01  
 PRIOR APPLICATION NUMBER: 60/190,479  
 PRIOR FILING DATE: 2000-03-17  
 PRIOR APPLICATION NUMBER: 60/200,545  
 PRIOR FILING DATE: 2000-04-27  
 PRIOR APPLICATION NUMBER: 60/200,303  
 PRIOR FILING DATE: 2000-04-28  
 PRIOR APPLICATION NUMBER: 60/200,779  
 PRIOR FILING DATE: 2000-04-28  
 PRIOR APPLICATION NUMBER: 60/200,999  
 PRIOR FILING DATE: 2000-05-01  
 PRIOR APPLICATION NUMBER: 60/202,084  
 PRIOR FILING DATE: 2000-05-04  
 PRIOR APPLICATION NUMBER: 60/206,201  
 PRIOR FILING DATE: 2000-05-22  
 PRIOR APPLICATION NUMBER: 60/218,950  
 PRIOR FILING DATE: 2000-07-14  
 PRIOR APPLICATION NUMBER: 60/222,903  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: 60/223,416  
 PRIOR FILING DATE: 2000-08-04  
 PRIOR APPLICATION NUMBER: 60/223,378  
 PRIOR FILING DATE: 2000-08-07  
 NUMBER OF SEQ ID NOS: 9597  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 2139  
 LENGTH: 110  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-796-692-2139

Query Match 14.9%; Score 32; DB 9; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-23;  
 Matches 32; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 169 HHPPSDHEATLRCWALGYPAAETITLWQDGE 200  
 Db 67 HHPPSDHEATLRCWALGYPAAETITLWQDGE 98

RESULT 12  
 US-10-040-862-799  
 Sequence 799, Application US/10040862  
 Publication No. US20030073396A1  
 GENERAL INFORMATION:  
 APPLICANT: Gaiger, Alexander  
 APPLICANT: Algate, Paul A.  
 APPLICANT: Rettter, Marc  
 APPLICANT: Corixa Corporation  
 TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
 FILE REFERENCE: 014058-013520US  
 CURRENT FILING DATE: 2001-11-06  
 PRIOR APPLICATION NUMBER: US 60/186,126  
 PRIOR FILING DATE: 2000-03-01  
 PRIOR APPLICATION NUMBER: US 60/190,479  
 PRIOR FILING DATE: 2000-03-17  
 PRIOR APPLICATION NUMBER: US 60/200,545  
 PRIOR FILING DATE: 2000-04-27  
 PRIOR APPLICATION NUMBER: US 60/206,201  
 PRIOR FILING DATE: 2000-04-28  
 PRIOR APPLICATION NUMBER: US 60/218,950  
 PRIOR FILING DATE: 2000-07-14  
 PRIOR APPLICATION NUMBER: US 60/222,903  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: US 60/223,416  
 PRIOR FILING DATE: 2000-08-04  
 PRIOR APPLICATION NUMBER: US 60/223,378

RESULT 13  
 US-10-040-862-2139  
 Sequence 2139, Application US/10040862  
 Publication No. US20030073396A1  
 GENERAL INFORMATION:  
 APPLICANT: Gaiger, Alexander  
 APPLICANT: Algate, Paul A.  
 APPLICANT: Mannion, Jane  
 APPLICANT: Rettter, Marc  
 APPLICANT: Corixa Corporation  
 TITLE OF INVENTION: Hematological Malignancies  
 FILE REFERENCE: 014058-013520US  
 CURRENT FILING DATE: 2001-11-06  
 PRIOR APPLICATION NUMBER: US 60/186,126  
 PRIOR FILING DATE: 2000-03-01  
 PRIOR APPLICATION NUMBER: US 60/190,479  
 PRIOR FILING DATE: 2000-03-17  
 PRIOR APPLICATION NUMBER: US 60/200,545  
 PRIOR FILING DATE: 2000-04-27  
 PRIOR APPLICATION NUMBER: US 60/206,201  
 PRIOR FILING DATE: 2000-04-28  
 PRIOR APPLICATION NUMBER: US 60/218,950  
 PRIOR FILING DATE: 2000-07-14  
 PRIOR APPLICATION NUMBER: US 60/222,903  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: US 60/223,416  
 PRIOR FILING DATE: 2000-08-04  
 PRIOR APPLICATION NUMBER: US 60/223,378

```

; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796, 692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 2139
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
us-10-040-822-2139                               Db      67 HHPISDHEATRCWALGFYPAEITLTWQDGE 98

; Query Match 14.9%; Score 32; DB 14; Length 110;
; Best Local Similarity 100.0%; Pred. No. 3.2e-23; Indels 0; Gaps 0;
; Matches 32; Conservative 0; Mismatches 0;

Qy   169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200
Db   67 HHPISDHEATLRCWALGFYPAEITLTWQDGE 98

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; of Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 20040002068A1
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/190,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 2139
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
us-10-057-475B-2139                               Db      67 HHPISDHEATRCWALGFYPAEITLTWQDGE 98

Query Match 14.9%; Score 32; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.2e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   169 HHPISDHEATRCWALGFYPAEITLTWQDGE 200
Db   67 HHPISDHEATRCWALGFYPAEITLTWQDGE 98

Search completed: July 13, 2005, 09:46:00
Job time : 94.5296 sec

```

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 13, 2005, 09:15:29 ; Search time 17.1472 Seconds  
(without alignments)

935.984 Million cell updates/sec

Title: US-09-819-371-6

Perfect score: 215

Sequence: 1 IAEVYVDDTQLRFDSAAI.....QRDGBEQTQDTTELLVTRPAG 215

Scoring table: OLIBGO

Gapext 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :	Issued Patents MA:*
1:	/cgcn2_6_ptodata/1/iaa/5A_COMBO.PEP:*
2:	/cgcn2_6_ptodata/1/iaa/5B_COMBO.PEP:*
3:	/cgcn2_6_ptodata/1/iaa/6A_COMBO.PEP:*
4:	/cgcn2_6_ptodata/1/iaa/6B_COMBO.PEP:*
5:	/cgcn2_6_ptodata/1/iaa/PCMS_COMBO.PEP:*
6:	/cgcn2_6_ptodata/1/iaa/backfile.PEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	11.9	55.3	362	4	US-09-949-016-8242	Sequence 8242, Ap
2	7.7	35.8	120	4	US-09-513-99C-4290	Sequence 4290, Ap
3	3.2	14.9	274	1	US-08-222-851-1	Sequence 1, Appl
4	2.8	13.0	358	4	US-09-949-016-6620	Sequence 6620, Ap
5	2.8	13.0	360	4	US-09-949-016-6370	Sequence 8310, Ap
6	1.7	7.9	184	3	US-09-153-586-21	Sequence 21, Appl
7	1.7	7.9	184	4	US-09-858-580-21	Sequence 9, Appl
8	1.6	7.4	117	2	US-08-406-057-9	Sequence 9, Appl
9	1.6	7.4	117	3	US-08-958-316-9	Sequence 8, Appl
10	1.6	7.4	145	2	US-08-406-057-8	Sequence 8, Appl
11	1.6	7.4	145	3	US-08-958-316-8	Sequence 8, Appl
12	1.6	7.4	338	4	US-09-949-016-8176	Sequence 6116, Ap
13	1.6	7.4	339	4	US-09-949-016-8636	Sequence 8636, Ap
14	1.6	7.4	361	3	US-08-652-265-22	Sequence 22, Appl
15	1.6	7.4	361	3	US-08-834-497A-22	Sequence 22, Appl
16	1.6	7.4	361	3	US-09-503-444A-22	Sequence 22, Appl
17	1.5	7.0	92	4	US-09-673-809-25	Sequence 25, Appl
18	1.5	7.0	182	1	US-08-127-954-135	Sequence 135, Appl
19	1.5	7.0	182	1	US-08-127-954-151	Sequence 151, Appl
20	1.5	7.0	274	2	US-08-484-005-105	Sequence 105, Appl
21	1.5	7.0	274	2	US-08-484-905-106	Sequence 106, Appl
22	1.5	7.0	274	2	US-08-484-905-107	Sequence 107, Appl
23	1.5	7.0	274	2	US-08-484-005-108	Sequence 108, Appl
24	1.5	7.0	274	3	US-08-481-985B-105	Sequence 105, Appl
25	1.5	7.0	274	3	US-08-481-985B-106	Sequence 106, Appl
26	1.5	7.0	274	3	US-08-481-985B-107	Sequence 107, Appl
27	1.5	7.0	274	3	US-08-481-985B-108	Sequence 108, Appl

RESULT 1

US-09-949-016-8242

; Sequence 8242, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949, 016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241, 755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237, 768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231, 498

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ For Windows Version 4.0

; SEQ ID NO: 8242

; LENGTH: 362

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-8242

Query Match 55.3%; Score 119; DB 4; Length 362;

Best Local Similarity 100.0%; Pred. No. 8.5e-111; Mismatches 0; Indels 0; Gaps 0;

Matches 119; Conservative 0; MisMatches 0;

Qy 97 DGKDYISLNEDLRSWTAADTVQITQFRYEAEFRPTYLEGECLELLRRLYENGKET 156

Db 140 DGKDYISLNEDLRSWTAADTVQITQFRYEAEFRPTYLEGECLELLRRLYENGKET 199

Qy 157 LQRADPPKAHVAAHPISDHEATCRWLALGFYPAPITLTWORDEEQTODTELVTRPAG 215

Db 200 LQRADPPKAHVAAHPISDHEATCRWLALGFYPAPITLTWORDEEQTODTELVTRPAG 258

RESULT 2

US-09-513-999C-4290

; Sequence 4290, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION

; APPLICANT: Dumas Milne Edwards, J.B.

; ATTORNEY: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59-US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24  
 PRIORITY APPLICATION NUMBER: US 60/1122,487  
 PRIOR FILING DATE: 1999-02-26  
 NUMBER OF SEQ ID NOS: 36681  
 SOFTWARE: Patent.pml  
 SEQ ID NO: 4290  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE: SIGNAL  
 NAME/KEY: SIGNAL  
 LOCATION: -17.-1  
 OTHER INFORMATION: score 9.3  
 OTHER INFORMATION: seq SLLLILSGALALT/DT  
 US-09-513-939C-4290

Query Match 35.8%; Score 77; DB 4; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 3e-69; Indels 0; Gaps 0;  
 Matches 77; Conservative 0; Mismatches 0;

Qy 1 IAVYVDTQFLRFDSDAIPMEPREMPEVWEEQGPQTWEITGYAKANAQTRVALRNLL 60  
 Db 44 IAVYVDTQFLRFDSDAIPMEPREMPEVWEEQGPQTWEITGYAKANAQTRVALRNLL 103

Qy 61 RRYNOSEAGSHTLQGMN 77  
 Db 104 RRYNQSEAGSHTLQGMN 120

RESULT 3  
 US-08-222-851-1  
 ; Sequence 1, Application US/08222851  
 GENERAL INFORMATION:  
 Patent No. 5723128  
 COMPUTER READABLE FORM:  
 ZIP: 20006-1812  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/222,851  
 FILING DATE: 05-APR-1994  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MILLMAN, ROBERT A.  
 REGISTRATION NUMBER: 36-217  
 REFERENCE/DOCKET NUMBER: 28600-20200.22  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 887-1500  
 TELEX: (100) 494-0792  
 INFORM FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 274 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: linear

Best Local Similarity 100.0%; Pred. No. 6.2e-24;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
 US-09-94-016-6620  
 ; Sequence 6620, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 6620  
 LENGTH: 358  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-94-016-6620

Query Match 13.0%; Score 28; DB 4; Length 358;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-20;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 HHPISDHEATLRCWALGFYPABITLTWORDGE 200  
 Db 191 HHPISDHEATLRCWALGFYPABITLTWORDGE 222

RESULT 5  
 US-09-94-016-8370  
 ; Sequence 8370, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 8370  
 LENGTH: 360  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-94-016-8370

Query Match 13.0%; Score 28; DB 4; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-20;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 HHPISDHEATLRCWALGFYPABITLTWO 196  
 |||||

Query Match 14.9%; Score 32; DB 1; Length 274;  
 US-08-222-851-1

Db 214 HHPISDHEATLRCWALGFPAAEITLTWQ 241  
**RESULT 6**  
US-09-153-586-21  
; Sequence 21, Application US/09153586A  
; Patent No. 627072  
; GENERAL INFORMATION:  
; APPLICANT: Burrows et al.  
; TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of  
; FILE REFERENCE: 48923  
; CURRENT APPLICATION NUMBER: US/09/153,586A  
; EARLIER APPLICATION NUMBER: 60/064,552  
; EARLIER FILING DATE: 1997-09-16  
; EARLIER APPLICATION NUMBER: 60/064,555  
; EARLIER FILING DATE: 1997-10-10  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 21  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-153-586-21

Query Match 7.9%; Score 17; DB 3; Length 184;  
Best Local Similarity 100.0%; Pred. No. 4.2e-09; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 146 LRRYLENGKETLQRADP 162  
Db 168 LRRYLENGKETLQRADP 184

RESULT 7  
US-09-858-580-21  
; Sequence 21, Application US/09858580  
; Patent No. 6815171  
; GENERAL INFORMATION:  
; APPLICANT: Burrows et al.  
; TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of  
; FILE REFERENCE: 48923  
; CURRENT APPLICATION NUMBER: US/09/858,580  
; CURRENT FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 09/153,586  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/064,552  
; PRIOR FILING DATE: 1997-09-16  
; PRIOR APPLICATION NUMBER: 60/064,555  
; PRIOR FILING DATE: 1997-10-10  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 21  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-858-580-21

Query Match 7.9%; Score 17; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 4.2e-09; Indels 0; Gaps 0;

Qy 146 LRRYLENGKETLQRADP 162  
Db 168 LRRYLENGKETLQRADP 184

RESULT 8  
US-08-406-057-9  
; Sequence 9, Application US/08406057  
; Patent No. 5856442  
; GENERAL INFORMATION:  
; APPLICANT: CAROSELLA, EDGARDO D  
; APPLICANT: MOREAU, PHILIPPE  
; APPLICANT: GLUCKMAN, ELIANE  
; APPLICANT: KIRSZENBAUM, MAREK  
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; ZIP: 22202  
; COMPUTER READABLE FORM:

Query Match 7.4%; Score 16; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2.8e-08; Mismatches 0; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 EATLRCWALGFYPAEI 191  
Db 20 EATLRCWALGFYPAEI 35

RESULT 9  
US-08-058-316-9  
; Sequence 9, Application US/08958316  
; Patent No. 6291659  
; GENERAL INFORMATION:  
; APPLICANT: CAROSELLA, EDGARDO D  
; APPLICANT: MOREAU, PHILIPPE  
; APPLICANT: GLUCKMAN, ELIANE  
; APPLICANT: KIRSZENBAUM, MAREK  
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; ZIP: 22202  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Tape  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/958,316  
 FILING DATE: 27-OCT-1997  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 94 03179  
 FILING DATE: 18-MAR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F  
 REGISTRATION NUMBER: 24,618  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEX: (703) 413-2220  
 TELEX: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 117 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-08-958-316-9

Query Match 7.4%; Score 16; DB 3; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;

Qy 176 EATLRCWALGFYPAEI 191  
 Db 20 EATLRCWALGFYPAEI 35

RESULT 10  
 US-08-106-057-8  
 Sequence 8, Application US/08406057  
 Patent No. 585642  
 GENERAL INFORMATION:  
 APPLICANT: CAROBELLA, EDGARDO D  
 APPLICANT: MOREAU, PHILIPPE  
 APPLICANT: GLUCKMAN, ELIANE  
 APPLICANT: KIRSZENBAUM, MAREK  
 TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
 CITY: ARLINGTON  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Tape  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/958,316  
 FILING DATE: 27-OCT-1997  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 94 03179  
 FILING DATE: 18-MAR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F  
 REGISTRATION NUMBER: 24,618  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEX: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 145 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-08-958-316-8

Query Match 7.4%; Score 16; DB 3; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;

RESULT 14  
 US-09-819-371-6.rai  
 Query 176 EATLRCWALGFYPAEI 191  
 Db 48 EATLRCWALGFYPAEI 63

RESULT 12  
 US-09-949-016-6176  
 ; Sequence 6176, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASES, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CLO001307  
 ; CURRENT APPLICATION NUMBER: US/09/949, 016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241, 755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237, 768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231, 498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSEQ For Windows Version 4.0  
 ; SEQ ID NO: 6176  
 ; LENGTH: 338  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-949-016-6176

Query Match 7.4%; Score 16; DB 4; Length 338;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 EATLRCWALGFYPAEI 191  
 Db 222 EATLRCWALGFYPAEI 237

RESULT 13  
 US-09-949-016-8636  
 ; Sequence 8636, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASES, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CLO001307  
 ; CURRENT APPLICATION NUMBER: US/09/949, 016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241, 755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237, 768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSEQ For Windows Version 4.0  
 ; SEQ ID NO: 8636  
 ; LENGTH: 339  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-949-016-8636

Query Match 7.4%; Score 16; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 EATLRCWALGFYPAEI 191  
 Db 223 EATLRCWALGFYPAEI 238

RESULT 15  
 US-08-652-265-22  
 ; Sequence 22, Application US/08652265  
 ; Patent No. 602530  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Thomas, Winston J.  
 ; APPLICANT: Drayna, Dennis T.  
 ; APPLICANT: Feder, John N.  
 ; APPLICANT: Gniurke, Andreas  
 ; APPLICANT: Ruddy, David  
 ; APPLICANT: Tsuchihashi, Zenta  
 ; APPLICANT: Wolff, Roger K.  
 ; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
 ; NUMBER OF SEQUENCES: 44  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/652,265  
 ; FILING DATE: 23-MAY-1996  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M.  
 ; REGISTRATION NUMBER: 30,223  
 ; REFERENCE DOCKET NUMBER: 17957-000500  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; INFORMATION FOR SEQ ID NO: 22:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 361 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FEATURE:  
 ; NAME/KEY: Protein  
 ; LOCATION: 1..361  
 ; OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"  
 ; US-08-652-265-22

Query Match 7.4%; Score 16; DB 3; Length 361;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 EATLRCWALGFYPAEI 191  
 Db 222 EATLRCWALGFYPAEI 237

RESULT 15  
 US-08-334-497A-22  
 ; Sequence 22, Application US/08834497A  
 ; Patent No. 6110305  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Thomas, Winston J.  
 ; APPLICANT: Drayna, Dennis T.  
 ; APPLICANT: Feder, John N.  
 ; APPLICANT: Gniurke, Andreas  
 ; APPLICANT: Ruddy, David  
 ; APPLICANT: Tsuchihashi, Zenta  
 ; APPLICANT: Wolff, Roger K.  
 ; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS  
 ; NUMBER OF SEQUENCES: 76

---

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Penne & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Polissari, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: Protein
FEATURE:
NAME KEY: Protein
LOCATION: 1..361
OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"
```

us-08-834-497A-22

```

Query Match
Best Local Similarity 7.4%; Score 16; DB 3; Length 361;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 176 EATLRCWALGFPAEI 191
          ||||| | | | | | | | |
Db 222 EATLRCWALGFPAEI 237
```

Result No.	Score	Query Match	Length	DB ID	Description
1	261	72.1	1	HLA_HUMAN	P30511; O9TP68;
2	245	67.7	346	2	Q8WLP5
3	244	67.4	460	2	Q95HCO
4	232	64.1	346	2	Q6DU28
5	223	61.6	324	2	Q861B9
6	223	61.6	324	2	Q861F0
7	196	54.1	254	2	Q860R0
8	196	54.1	346	2	Q8MGQ1
9	174	48.1	346	2	Q6DU20
10	148	40.9	349	2	Q6ZDWO
11	113	31.2	346	1	1C28_PANTR
12	113	31.2	346	2	Q95IT2
13	113	31.2	362	1	Q7YR27
14	87	24.0	91	2	Q9TPX7
15	73	20.2	316	2	Q29958
16	62	17.1	314	2	Q860F6
17	61	16.9	353	2	Q9MXS6
18	61	16.9	353	2	Q9MXS7
19	61	16.9	354	2	Q70UE5
20	61	16.9	354	2	Q70UE6
21	61	16.9	354	2	Q70UE7
22	61	16.9	365	2	Q6GST5
23	61	16.9	365	2	Q9MXS5
24	59	16.3	59	2	Q78094
25	58	16.3	348	1	HLA_MACMU
26	58	16.0	354	2	Q70ST0
27	58	16.0	365	2	Q6IT7A3
28	55	15.2	365	2	Q6IT7A9
29	53	14.6	354	2	Q70SH4
30	53	14.6	365	2	Q6IT796
31	50	13.8	351	2	Q70PL7

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model.

Run on: July 13, 2005, 08:59:16 ; Search time 169 Seconds  
(without alignments)

1096.880 Million cell updates/sec

Title: US-09-819-371-4

Perfect score: 362

Sequence: 1 MAPRSLLLSSGALALTDTW.....QQAVTDSAQGSGVSLTANKV 3 62

Scoring table: Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt\_03:  
1: uniprot\_sprot:  
2: uniprot\_trembl:  
\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT 1		HLA_HUMAN		STANDARD:	
ID	P30511; O9TP68;	AC	P30511; O9TP68;	PRY:	362 AA.
DT	01-APR-1993 (Rel. 25, Created)	DT	01-APR-1993 (Rel. 25, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)	DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DB	HLA Class I Histocompatibility antigen, alpha chain F precursor (HLA F antigen) (Leukocyte antigen F) (CD12).	DB	HLA Class I Histocompatibility antigen, alpha chain F precursor (HLA F antigen) (Leukocyte antigen F) (CD12).		
DB	Name=HLA-F; Synonyms=HLA-5,4, HLA-F;	DB	Name=HLA-F; Synonyms=HLA-5,4, HLA-F;		
GN	Homo sapiens (Human).	GN	Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_TaxID	9606;	NCBI_TaxID	9606;		
RN	SEQUENCE FROM N.A. MEDLINE=90111605; PubMed=1688605;	RN	SEQUENCE FROM N.A. MEDLINE=90111605; PubMed=1688605;		
RX	Geraghty D.B., Wei X., Orr H.T., Koller B.H.;	RX	Geraghty D.B., Wei X., Orr H.T., Koller B.H.;		
RT	"Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive element.";	RT	"Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive element.";		
RL	J. Exp. Med. 171:1-18(1990).	RL	J. Exp. Med. 171:1-18(1990).		
RN	[2]	RN	[2]		
RP	SEQUENCE FROM N.A. MEDLINE=91197889; PubMed=1707659;	RP	SEQUENCE FROM N.A. MEDLINE=91197889; PubMed=1707659;		
RX	Lury D., Epstein H., Holmes N.;	RX	Lury D., Epstein H., Holmes N.;		
RA	The human class I MHC gene HLA-F is expressed in lymphocytes.;	RA	The human class I MHC gene HLA-F is expressed in lymphocytes.;		
RT	Int. Immunol. 2:531-531(1990).	RT	Int. Immunol. 2:531-531(1990).		
RN	[3]	RN	[3]		
RP	SEQUENCE FROM N.A. MEDLINE=2018617; PubMed=10727063;	RP	SEQUENCE FROM N.A. MEDLINE=2018617; PubMed=10727063;		
RX	Hanpe A., Coritton O., Andrieux N., Carn G., Lepourcet M., Galibert F.;	RX	Hanpe A., Coritton O., Andrieux N., Carn G., Lepourcet M., Galibert F.;		
RA	"A 356-Rb sequence of the subtelomeric part of the MHC class I region.",	RA	"A 356-Rb sequence of the subtelomeric part of the MHC class I region.",		
RT	RT	RT	RT		
RT	Dreano S., Gatus M.T., Hitte C., Soriano N., Galibert F.;	RT	Dreano S., Gatus M.T., Hitte C., Soriano N., Galibert F.;		
RN	DNA Seq. 10:263-299(1999).	RN	DNA Seq. 10:263-299(1999).		
RP	SEQUENCE FROM N.A. RA	RP	SEQUENCE FROM N.A. RA		
RX	Shina S., Tamai Y., Oka A., Inoko H.;	RX	Shina S., Tamai Y., Oka A., Inoko H.;		
RA	"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";	RA	"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";		
RT	Submitted (SPR-1999) to the EMBL/GenBank/DBJ databases.	RT	Submitted (SPR-1999) to the EMBL/GenBank/DBJ databases.		
RL	[5]	RL	[5]		
RP	SEQUENCE FROM N.A. AND VARIANT PRO-272.	RP	SEQUENCE FROM N.A. AND VARIANT PRO-272.		
RX	MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;	RX	MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;		
RA	Murgall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L., Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E., Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainough R., Ambroze K.D., Andrews T.D., Ashwell R.I.S., Bainbridge A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J., Barlow K.P., Bates K., Bearne D.M., Beasley O., Bird C.P., Bray-Aiken S.E., Brook J., Brown A.J., Brown J.Y., Burford D.C., Burrow J., Carter C., Carter N.P., Chapman J.C., Clark S.Y., Clark G., Cleee C.M., Cobley V., Collier R.E., Collins J.E., Coiman L.K., Corby N.R., Coville G.J.,	RA	Murgall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L., Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E., Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainough R., Ambroze K.D., Andrews T.D., Ashwell R.I.S., Bainbridge A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J., Barlow K.P., Bates K., Bearne D.M., Beasley O., Bird C.P., Bray-Aiken S.E., Brook J., Brown A.J., Brown J.Y., Burford D.C., Burrow J., Carter C., Carter N.P., Chapman J.C., Clark S.Y., Clark G., Cleee C.M., Cobley V., Collier R.E., Collins J.E., Coiman L.K., Corby N.R., Coville G.J.,		



- |          |   |   |
|----------|---|---|
| QY       | 61  | AATIRMEPREPWPBQECPQWETWTGAYAKANAQTDRVALNLRLRNQSEASHTLQGMN 120           |
| RA       | Brownstein M.J., Usdin T.B., Tohiyuki S., Casavant T.L., Scheetz T.B., Loqueilano N.A., Peters G.J., Abramson R.D., Mulilay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia P., Yabeyae F., Villalon D.K., Muñiz D.M., Sodergren E.J., Lu X., Gibbs R.A., Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green D., Dickson M.C., Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smialus D.E., Schniech A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." / Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [15]   |   |
| RA       | RP  | SEQUENCE FROM N.A.  |
| RA       | RC  | TISSUE=lymph;   |
| RA       | RA  | Straubberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. |
| RN       | RN  | [6]   |
| RP       | SEQUENCE FROM N.A.  |   |
| RA       | Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.   |   |
| RN       | RN  | [16]  |
| RP       | SEQUENCE FROM N.A.  |   |
| RA       | Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.   |   |
| RN       | RN  | [16]  |
| RESULT 3 | Q99HC0  | PRELIMINARY;  |
| ID       | Q99HC0;   | PRT;  |
| AC       | Q99HC0;   | 460 AA.   |
| DT       | 01-DEC-2001 (TREMBLrel. 19, Created)  |   |
| DT       | 01-MAR-2004 (TREMBLrel. 26, Last annotation update)   |   |
| DE       | HUA-F protein (Fragment).   |   |
| GN       | Name=HUA_F;   |   |
| OS       | <i>Homo sapiens</i> (Human).  |   |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  |   |
| OC       | NCBI_TaxID=9606;  |   |
| OX       |   |   |
| RN       | SEQUENCE FROM N.A.  |   |
| RP       | TISSUE=lung;  |   |
| RX       | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  |   |
| RA       | Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heisler F., Diatchenko L., Matsunaga K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Yoshiuki S., Carninci P., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullah S.J., Bosak S.A., McBryan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton B., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smialus D.E., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." / Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [12] |   |
| RP       | SEQUENCE FROM N.A.  |   |
| RA       | Straubberg R.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.   |   |
| DR       | EMBL; BC009260; AAH09260..2; -  |   |
| DR       | HSSP; Q9TQH5; 1BOR.   |   |
| RA       | SEQUENCE FROM N.A.  |   |
| RA       | Straubberg R.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.   |   |
| DR       | EMBL; BC009260; AAH09260..2; -  |   |
| DR       | GO; GO:0006955; P:immune response; IEA.   |   |
| DR       | InterPro; IPR003597; Ig-like.   |   |
| DR       | InterPro; IPR003597; Ig-cl.   |   |
| DR       | InterPro; IPR003006; Ig_MHC.  |   |
| DR       | InterPro; IPR001039; MHC_I.   |   |
| DR       | Pfam; PF00754; Cl-set.  |   |
| DR       | PRINTS; PRO1638; MHCIASSI.  |   |
| DR       | ProDom; P000050; MHC_I; 1.  |   |
| DR       | DR SMART; SM0407; IgC1; 1.  |   |
| DR       | DR PROSITE; PS00835; Ig_LIKE; 1.  |   |
| DR       | DR PROSITE; PS00290; Ig_MHC; 1.   |   |
| RN       | SEQUENCE FROM N.A.  |   |
| RA       | Score 245; DB 2; Length 346;  |   |
| RA       | Best Local Similarity 99.7%; Pred. No. 9_2e-228;  |   |
| RA       | Matches 345; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  |   |
| RA       | 1 MAPRSLLLSGALLTDTWAGSHSLRYFSTAVSRGRGEPRYIAVEYVDTQFLREDSD 60  |   |
| RA       | 1 MAPRSLLLSGALLTDTWAGSHSLRYFSTAVSRGRGEPRYIAVEYVDTQFLREDSD 60  |   |
| QY       | 1 MAPRSLLLSGALLTDTWAGSHSLRYFSTAVSRGRGEPRYIAVEYVDTQFLREDSD 60  |   |
| Db       | 1 MAPRSLLLSGALLTDTWAGSHSLRYFSTAVSRGRGEPRYIAVEYVDTQFLREDSD 60  |   |



Db	61 RMEPREPWEQGPQYNEWTTGAKANAQTDRVALRNLLRYNQSEAGSHTLOGNGCDM 120	Db	181 CLELLRLYLENGKETLQRADPPKAHVAAHPISDHEATLRCWALGFYPABITLTWORDGEE 240
Qy	125 GPDGRLLRGTHQAYDGKDYISLNEDLSRSTAADTVQITQRFYEAEEFRYILEG 184	Qy	245 QTQDTELVELTRPAGDTFQKWAAYVVPSGEQRFTCHVQEGLPQLLRLWEQSQOPTIP 304
Db	121 GPDGRLLRGTHQAYDGKDYISLNEDLSRSTAADTVQITQRFYEAEEFRYILEG 180	Db	241 QTQDTELVELTRPAGDTFQKWAAYVVPSGEQRFTCHVQEGLPQLLRLWEQSQOPTIP 300
Qy	185 CLELLRLYLENGLETQRADPPKAHVAAHPISDHEATLRCWALGFYPABITLTWORDGEE 244	Qy	305 IVGIVAGLVVLGAUVTGAVVAAVM 328
Db	181 CLELLRLYLENGLETQRADPPKAHVAAHPISDHEATLRCWALGFYPABITLTWORDGEE 240	Db	301 IVGIVAGLVVLGAUVTGAVVAAVM 324
Qy	245 QTQDTELVELTRPAGDTFQKWAAYVVPSGEQRFTCHVQEGLPQLLRLWEQSQOPTIP 304	RESULT 7	
Db	241 QTQDTELVELTRPAGDTFQKWAAYVVPSGEQRFTCHVQEGLPQLLRLWEQSQOPTIP 300	Q86R00	PRELIMINARY;
Qy	305 IVGIVAGLVVLGAUVTGAVVAAVM 328	ID Q86R00;	PRT; 254 AA.
Db	301 IVGIVAGLVVLGAUVTGAVVAAVM 324	AC Q86R00;	
RESULT 6			
Q861FO	PRELIMINARY;	PRT;	324 AA.
AC	Q861FO;	PRT;	
DT	01-JUN-2003 (TREMBrel. 24, Created)	DT	01-JUN-2003 (TREMBrel. 24, Created)
DT	01-MAR-2004 (TREMBrel. 26, Last annotation update)	DT	01-MAR-2004 (TREMBrel. 24, Last sequence update)
DE	Nonclassical MHC class I antigen (Fragment).	DT	01-MAR-2004 (TREMBrel. 26, Last annotation update)
GN	Name=HLA-F;	RA	Liu Y., He X., Xu L., Zeng Y.;
OS	Homo sapiens (Human).	RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	DR	EMBL; AV253271; AR086775.1;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	RN	GO; GO:0016030; C:membrane; IEA.	
NCBI_TaxID=9606;	[1]	DR	GO; GO:0006935; P:immune response; IEA.
RN	RP	DR	InterPro; IPR001039; MHC_I.
RA	SEQUENCE FROM N.A.	DR	Pfam; PF00129; MHC_I; 1.
XU	Xu L., Liu Y., Zeng Y.	DR	PRINTS; PRO1638; MHCC1.LSSI.
RL	Submitted (JAN 2003) to the EMBL/GenBank/DBJ databases.	DR	PRODOM; PD000050; MHC_I; 1.
DR	AV216682; AA037689.1; -.	SQ	SEQUENCE 254 AA; 2888 MW; C81F225D409AAED2 CRC64;
HSSP	Q9TOH5; 1B0R.	Query Match	Best Local Similarity 10.0%; Pred. No. 1.e-180;
DR	GO; GO:0016020; C:membrane; IEA.	Matches	196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	InterPro; IPR007110; Ig-like.	Qy	1 MAPSSLLLSGALALTDTWAGSHSLRFSTAVSRPGCPEPRYIAVEVYDDTQTLRFDSD 60
DR	IPR03597; Ig_C1.	Db	1 MAPSSLLLSGALALTDTWAGSHSLRFSTAVSRPGCPEPRYIAVEVYDDTQTLRFDSD 60
DR	IPR03006; Ig_MHC.	DR	61 AAERFMEPREPWYEQGPQYWTTGAKANAQTDRLRNLIRYNOEAGSHTLQGMN 120
DR	IPR001039; MHC_I.	DR	61 AAERFMEPREPWYEQGPQYWTTGAKANAQTDRLRNLIRYNOEAGSHTLQGMN 120
DR	Pfam; PF007654; Cl-set; 1.	Qy	121 GCDMPDGSRLRGYHQAYDGKDYISLNEDLRSWTAADTVQITQRFYEAEEFRYI 180
DR	PRINTS; PRO1638; MHCC1.LSSI.	Db	121 GCDMPDGSRLRGYHQAYDGKDYISLNEDLRSWTAADTVQITQRFYEAEEFRYI 180
DR	PRODOM; PD000050; MHC_I; 1.	Qy	181 LEGECLELRRLYENG 196
DR	SMART; SM00407; Ig_C1.	Db	181 LEGECLELRRLYENG 196
DR	PROSITE; PS50835; IG_LIKE; 1.	Qy	181 LEGECLELRRLYENG 196
DR	PROSITE; PS00290; Ig_MHC; 1.	Db	181 LEGECLELRRLYENG 196
FT	NON_TER 1 324	SEQUENCE	324 AA; 36518 MW; E3E028177D2716F4 CRC64;
SQ	Score 61. 6%; Best Local Similarity 99. 7%; Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 8	
Qy	5 SLLLSGALALTDTWAGSHSLRFSTAVSRPGCPEPRYIAVEVYDDTQTLRFDSDAIP 64	Q8MGQ1	PRELIMINARY;
Db	1 SLLLSGALALTDTWAGSHSLRFSTAVSRPGCPEPRYIAVEVYDDTQTLRFDSDAIP 60	ID Q8MGQ1;	PRT; 346 AA.
Qy	65 RMEPREPWEQGPQYWTTGAKANAQTDRLRNLIRYNOEAGSHTLQGMNGCDM 124	AC Q8MGQ1;	
Db	61 RMEPREPWEQGPQYWTTGAKANAQTDRLRNLIRYNOEAGSHTLQGMNGCDM 120	DT 01-OCT-2002 (TREMBrel. 22, Created)	
Qy	125 GPDGRLLRGTHQAYDGKDYISLNEDLSRSTAADTVQITQRFYEAEEFRYILEG 184	DT 25-OCT-2004 (TREMBrel. 28, Last sequence update)	
Db	121 GPDGRLLRGTHQAYDGKDYISLNEDLSRSTAADTVQITQRFYEAEEFRYILEG 180	DB MHC Class Ib antigen.	
Qy	185 CLELLRLYLENGLETQRADPPKAHVAAHPISDHEATLRCWALGFYPABITLTWORDGEE 244	OS Homo sapiens (Human).	
Db		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
Qy		OX NCBI_TaxID=9606;	
		RN [1] SEQUENCE FROM N.A.	

Sequence Comparison Results						
	Query Sequence			Target Sequence		
	Qry	Db	Qry	Db	Qry	Db
RA	Ishitanii A., Miki A., Williams L.M., Moore Y., Geraghty D.E.; Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.	[2]				
RA	SEQUENCE FROM N.A.					
RA	Pyo C.-W., Ishitanii A., Moore Y.F., Geraghty D.E.; Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	[2]				
DR	EMBL; AF522284; AAM74479.1; -.	DR	EMBL; AF522291; AAM74486.1; -.	DR	EMBL; AF522292; AAM74487.1; -.	DR
DR	EMBL; AY645748; AAT73231.1; -.	DR	EMBL; AY645754; AAT72337.1; -.	DR	HSSP; Q9TOH5; 1B0R.	DR
DR	GO; GO:0016021; C:integral to membrane; IEA.	DR	GO; GO:0009550; P:immune response; IEA.	DR	InterPro; IPR007110; Ig-like.	DR
DR	InterPro; IPR003597; Ig-cl.	DR	InterPro; IPR003606; Ig-MHC.	DR	InterPro; IPR001039; MHC_I.	DR
DR	Pfam; PF07654; Cl-set; 1.	DR	Pfam; PF001229; MHC_I.	DR	PRINTS; PRO1638; MHCCASSI.	DR
DR	PRINTS; PRO00050; MHC_I.	DR	PROSITE; SM00407; IgCl_1.	DR	PROSITE; PS50835; Ig_IKE; 1.	DR
DR	PROSITE; FS00290; Ig_MHC; 1.	KW	Transmembrane.	SQ	SEQUENCE 346 AA; 39061 MW; D4782968A67E9B7D CRC64;	
Query Match Score 54.1%; Best Local Similarity 100.0%; Length 346; Matches 196; Conservative 0; Mismatches 0; Indels 0						
Qy	1 MAPRSLLLGGALATDTWAGSHSLRYFSTAVSRPGRGPRTAYVEVYDDT	1 MAPRSLLLGGALATDTWAGSHSLRYFSTAVSRPGRGPRTAYVEVYDDT	1 MAPRSLLLGGALATDTWAGSHSLRYFSTAVSRPGRGPRTAYVEVYDDT	1 MAPRSLLLGGALATDTWAGSHSLRYFSTAVSRPGRGPRTAYVEVYDDT	1 MAPRSLLLGGALATDTWAGSHSLRYFSTAVSRPGRGPRTAYVEVYDDT	1 MAPRSLLLGGALATDTWAGSHSLRYFSTAVSRPGRGPRTAYVEVYDDT
Qy	61 AAIPRMEDPREPWEQEQQPOYWWTGTYKANQATDVRALRNLLRYNQSEG	61 AAIPRMEDPREPWEQEQQPOYWWTGTYKANQATDVRALRNLLRYNQSEG	61 AAIPRMEDPREPWEQEQQPOYWWTGTYKANQATDVRALRNLLRYNQSEG	61 AAIPRMEDPREPWEQEQQPOYWWTGTYKANQATDVRALRNLLRYNQSEG	61 AAIPRMEDPREPWEQEQQPOYWWTGTYKANQATDVRALRNLLRYNQSEG	61 AAIPRMEDPREPWEQEQQPOYWWTGTYKANQATDVRALRNLLRYNQSEG
Qy	121 GCDMGPDRGLLRGHQHADKGDYTLISNEQLRSTAADTVQAITORFYEAEE	121 GCDMGPDRGLLRGHQHADKGDYTLISNEQLRSTAADTVQAITORFYEAEE	121 GCDMGPDRGLLRGHQHADKGDYTLISNEQLRSTAADTVQAITORFYEAEE	121 GCDMGPDRGLLRGHQHADKGDYTLISNEQLRSTAADTVQAITORFYEAEE	121 GCDMGPDRGLLRGHQHADKGDYTLISNEQLRSTAADTVQAITORFYEAEE	121 GCDMGPDRGLLRGHQHADKGDYTLISNEQLRSTAADTVQAITORFYEAEE
Qy	181 LEGCCELELLRRYLENG 196	181 LEGCCELELLRRYLENG 196	181 LEGCCELELLRRYLENG 196	181 LEGCCELELLRRYLENG 196	181 LEGCCELELLRRYLENG 196	181 LEGCCELELLRRYLENG 196
DB	OS Homo sapiens (Human).	OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi.	OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	NCBI_TAXID=9606;	[1]	
RP	SEQUENCE FROM N.A.					
RA	Pyo C.-W., Ishitanii A., Moore Y.F., Geraghty D.E.; Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	[2]				
DR	EMBL; AY645755; AAT73238.1; -.	DR	GO; GO:0016020; C:membrane; IEA.	DR	InterPro; IPR007110; Ig-like.	DR
DR	GO; GO:0006555; P:immune response; IEA.	DR	InterPro; IPR003597; Ig-cl.	DR	InterPro; IPR001039; MHC_I.	DR
DR	InterPro; IPR003007; Ig_MHC.					

Query Match	40.9%	Score 148;	DB 2;	Length 349;					
Best Local Similarity	100.0%	Pred. No.	4.9e-134;						
Matches	148;	Conservative	0;	Nismatches	0;	Indels	0;	Gaps	0;
Qy	198	ETLORADPPKAHHPISDHEATLRCWALGFYPAETTLWQDGEBOEQDTTELVETRPA	257						
Db	112	ETLORADPPKAHHPISDHEATLRCWALGFYPAETTLWQDGEBOEQDTTELVETRPA	171						
Qy	258	GDTGFKWQKAVVVPSGEORYTCHVQHELPOPILRLNEQSPOPTIPVGIVAGLVVGA	317						
Db	172	GDTGFKWQKAVVVPSGEORYTCHVQHELPOPILRLNEQSPOPTIPVGIVAGLVVGA	231						
Qy	318	WVTGAVVAAVMWKKSSDNRGSYQAA	345						
Db	232	WVTGAVVAAVMWKKSSDNRGSYQAA	259						
<hr/>									
RESULT 11									
ID	1C28_PANTR	STANDARD;	PRT;	346 AA.					
AC	P16215;								
DT	01-APR-1990	(Rel. 14, Created)							
DT	01-APR-1990	(Rel. 14, Last sequence update)							
DE	CHIA class I histocompatibility antigen, CH28 alpha chain precursor.								
OS	Pan troglodytes (Chimpanzee)								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;								
OX	NCBI_TaxID:9598;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE-90201944; PubMed=16590682;								
RA	Lawlor D.A., Warren E., Ward F.B., Parham P.; Buteleostomi; Pan.								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RA	MEDLINE-88319000; PubMed=34112487; DOI=10.1038/335268a0;								
RT	"HLA and B polymorphisms predate the divergence of humans and chimpanzees."								
RL	Nature 335:268-271(1988).								
CC	-I - FUNCTION: Involved in the presentation of foreign antigens to the immune system.								
CC	-I - SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).								
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).								
CC	DR	HSPB; Q29961; IBSA.							
CC	DR	InterPro; IPR00710; Ig-like.							
CC	DR	InterPro; IPR003597; Ig_C1.							
CC	DR	InterPro; IPR003006; Ig_MHC.							
CC	DR	InterPro; IPR001039; MHC_I.							
CC	PFam; PF00047; Ig_1.								
CC	DR	InterPro; IPR00129; MHC_I.							
CC	DR	PRINTS; PRO1638; MHCLASSI.							
CC	DR	PRODom; PD000050; MHC_I.							
CC	DR	SMART; SM00405; Ig_MHC.							
CC	DR	PROSITE; PS50835; Ig_LIKE.							
CC	DR	PROSITE; PS00290; Ig_MHC.							
CC	KW	Transmembrane.							
CC	DR	SEQUENCE 346 AA;							
CC	DR	Score 113; DB 2;							
CC	DR	Length 346;							
CC	DR	Best Local Similarity 100.0%;							
CC	DR	Pred. No. 3.2e-100;							
CC	DR	Mismatches 0;							
CC	DR	Indels 0;							
CC	DR	Gaps 0;							
Qy	198	TTGYAKANAQTDRVVALNLRRYNOSEAGNSHTLQGMNCDDMGPDGRLLRGYHQHAYDGSKD	143						
Db	84	TTGYAKANAQTDRVVALNLRRYNOSEAGNSHTLQGMNCDDMGPDGRLLRGYHQHAYDGSKD	143						
Qy	84	TTGYAKANAQTDRVVALNLRRYNOSEAGNSHTLQGMNCDDMGPDGRLLRGYHQHAYDGSKD	143						
Db	84	TTGYAKANAQTDRVVALNLRRYNOSEAGNSHTLQGMNCDDMGPDGRLLRGYHQHAYDGSKD	143						
Qy	144	YISLNEDLRSWTAADTVQITQRFYEAEYAEFRTYLEGECLELLRYLENG	196						
Db	144	YISLNEDLRSWTAADTVQITQRFYEAEYAEFRTYLEGECLELLRYLENG	196						



Qy	216	SDHEATLRCWALGFYPAEITLTWORDGEETQDTELVETRAGDTFQKWAAYVVPSGEB	275
Db	169	SDHEATLRCWALGFYPAEITLTWORDGEETQDTELVETRAGDTFQKWAAYVVPSGEB	228
Qy	276	QRYTCHVQHGLP	288
Db	229	QRYTCHVQHGLP	241

Search completed: July 13, 2005, 09:11:49  
Job time : 171 secs

**THIS PAGE BLANK (USPTO)**

Result No.	Score	Query Match	Length DB	ID	Description
1	250	91.2	362	4	US-09-949-016-8242 Sequence 8242, App
2	99	36.1	120	4	US-09-513-99C-4290 Sequence 4290, App
3	44	16.1	274	1	US-08-222-851-1 Sequence 1, App1
4	43	15.7	358	4	US-09-949-016-6620 Sequence 6620, App
5	43	15.7	360	4	US-09-949-016-8370 Sequence 8370, App
6	39	14.2	117	3	US-08-405-316-9 Sequence 9, App1
7	39	14.2	117	3	US-08-405-316-9 Sequence 9, App1
8	39	14.2	145	2	US-08-406-057-8 Sequence 8, App1
9	39	14.2	145	2	US-08-406-057-8 Sequence 8, App1
10	39	14.2	338	4	US-09-949-016-6176 Sequence 6176, App
11	39	14.2	339	4	US-09-949-016-8636 Sequence 8636, App
12	30	10.9	289	3	US-08-481-985B-105 Sequence 79, App1
13	30	10.9	289	3	US-08-481-985B-79 Sequence 79, App1
14	30	10.9	289	3	US-08-370-476-79 Sequence 105, App1
15	29	10.6	274	2	US-08-484-905-105 Sequence 107, App1
16	29	10.6	274	2	US-08-484-905-107 Sequence 107, App1
17	29	10.6	274	2	US-08-484-905-108 Sequence 108, App1
18	29	10.6	274	3	US-08-481-985B-105 Sequence 107, App1
19	29	10.6	274	3	US-08-481-985B-107 Sequence 107, App1
20	29	10.6	274	3	US-08-481-985B-108 Sequence 108, App1
21	29	10.6	274	3	US-08-370-476-105 Sequence 105, App1
22	29	10.6	274	3	US-08-370-476-107 Sequence 107, App1
23	29	10.6	274	3	US-08-370-476-108 Sequence 108, App1
24	29	10.6	341	3	US-08-890-719-38 Sequence 38, App1
25	29	10.6	365	2	US-08-484-905-97 Sequence 97, App1
26	29	10.6	365	2	US-08-484-905-98 Sequence 98, App1
27	29	10.6	365	2	US-08-484-905-99 Sequence 99, App1

RESULT 2  
 US-09-513-999C-4290  
 Sequence 4290 Application US/09513999C  
 GENERAL INFORMATION:  
 Patent No. 6783961  
 APPLICANT: Dumas Milne Edwards, J.B.  
 DUCLERT, A.  
 APPLICANT: Giordano, J.Y.  
 TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 Patent No. 6783961  
 FILE REFERENCE: 59.US2.REG  
 CURRENT APPLICATION NUMBER: US/09/513,999C  
 CURRENT FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: US 60/122,487  
 PRIOR FILING DATE: 1999-02-26  
 NUMBER OF SEQ ID NOS: 36681  
 SOFTWARE: Patent .pm  
 SEQ ID NO: 4290  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SIGNAL  
 LOCATION: -17.-1  
 OTHER INFORMATION: score 9.3  
 OTHER INFORMATION: seq SLLLISGALALT/DT  
 US-09-513-999C-4290

Query Match 36.1%; Score 99; DB 4; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-90;  
 Matches 99; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GSHSLRYFSTAVSRPGRGEPRVIAVEVDDTFLRFLPSDAALPRMEPRREPVEQEGPQYW 60  
 Db 22 GSHSLRYFSTAVSRPGRGEPRVIAVEVDDTFLRFLPSDAALPRMEPRREPVEQEGPQYW 81

Query Match 36.1%; Score 99; DB 4; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-90;  
 Matches 99; Conservative 0; Mismatches 0; Gaps 0;

Qy 61 EMTTGAYKANACTDVRALRNLLRRYNOSEAGSHTLQMN 99  
 Db 82 EMTTGAYKANACTDVRALRNLLRRYNOSEAGSHTLQMN 120

RESULT 3  
 US-09-222-851-1  
 Sequence 1, Application US/09222851  
 GENERAL INFORMATION:  
 Patent No. 5733128  
 APPLICANT: CLAVERGER, CAROL A.  
 APPLICANT: KRENSKY, ALAN M.  
 APPLICANT: PARHAM, PETER  
 TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: MORRISON & FOERSTER  
 STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20006-1812  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/222,851  
 FILING DATE: 05-APR-1994  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MILLMAN, ROBERT A.  
 REGISTRATION NUMBER: 36,217  
 REFERENCE/DOCKET NUMBER: 28600-20200.22  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500  
 TELEFAX: (202) 494-0792  
 TELEX: 90-4030 MRSNPFERSWH  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 274 amino acids  
 TYPE: amino acid  
 STRANDBEDNESS: single  
 TOPSOLOGY: linear  
 US-09-222-851-1

Query Match 16.1%; Score 44; DB 1; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-35;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQDTVELVTRPAGDTFQKWAAYVVPSGEEQRTCHVQHEGLP 267  
 Db 224 QTQDTVELVTRPAGDTFQKWAAYVVPSGEEQRTCHVQHEGLP 267

RESULT 4  
 US-09-949-016-6620  
 Sequence 6620, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSBQ for Windows Version 4.0  
 ; SEQ ID NO 6620  
 ; LENGTH: 358  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-949-016-6620

Query Match 15.7%; Score 43; DB 4; Length 358;  
 Best Local Similarity 100.0%; Pred. No. 2e-34;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 225 QTQDTVELVTRPAGDTFQKWAAYVVPSGEEQRTCHVQHEGLP 267  
 Db 246 QTQDTVELVTRPAGDTFQKWAAYVVPSGEEQRTCHVQHEGLP 268

RESULT 5  
 US-09-949-016-8370  
 Sequence 8370, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSBQ for Windows Version 4.0

SEQ ID NO: 8370  
 LENGTH: 360  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016: 8370

Query Match 15.7%; Score 43; DB 4; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 2e-34;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 225 TDQTTELVETRPGDGTFKWAAVVPSPGEEQRVTCHVQHEGLP 267  
 Db 248 TDQTTELVETRPGDGTFKWAAVVPSPGEEQRVTCHVQHEGLP 290

RESULT 6  
 US-08-406-057-9  
 Sequence 9, Application US/08406057  
 GENERAL INFORMATION:  
 APPLICANT: CAROSELLA, EDGARDO D  
 APPLICANT: MOREAU, PHILIPPE  
 APPLICANT: GLUCKMAN, ELINE  
 APPLICANT: KIRSZENBAUM, MAREK  
 TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
 NUMBER OF SEQUENCES: 1-7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Tape  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/958.316  
 FILING DATE: 27-OCT-1997  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 REFERENCE/DOCKET NUMBER: 0846-0437-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEFAX: (703) 413-2220  
 NAME: OBLON, NORMAN F  
 REGISTRATION NUMBER: 24,618  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 117 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-958-316-9

Query Match 14.2%; Score 39; DB 3; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-31;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 ELVETRPGDGTQKWAAVVPGEEQRVTCHVQHEGLP 267  
 Db 51 ELVETRPGDGTQKWAAVVPGEEQRVTCHVQHEGLP 89

RESULT 8  
 US-08-406-057-8  
 Sequence 8, Application US/08406057  
 Patent No. 5856442  
 GENERAL INFORMATION:  
 APPLICANT: CAROSELLA, EDGARDO D  
 APPLICANT: MOREAU, PHILIPPE  
 APPLICANT: GLUCKMAN, ELINE  
 APPLICANT: KIRSZENBAUM, MAREK  
 TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
 NUMBER OF SEQUENCES: 1-5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
 CITY: ARLINGTON  
 STATE: VIRGINIA

COUNTRY: USA  
 ZIP: 2202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Tape  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/406,057  
 FILING DATE: 17-MAR-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 94 03179  
 FILING DATE: 18-MAR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F  
 REGISTRATION NUMBER: 24,618  
 REFERENCE DOCKET NUMBER: 846-331-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEX: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 145 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-406-057-8

Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.2e-31;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 ELVETRPGDGTFQKWAAYVPSGEQRTCHVQHEGLP 267  
 Db 79 ELVETRPGDGTFQKWAAYVPSGEQRTCHVQHEGLP 117

RESULT 9  
 US-08-958-316-8  
 Sequence 8, Application US/0858316  
 Patent No. 6231659

GENERAL INFORMATION:  
 APPLICANT: CAROSELLA, EDGARDO D  
 APPLICANT: MOREAU, PHILIPPE  
 APPLICANT: GLUCKMAN, ELLIANE  
 APPLICANT: KIRSZENBAUM, MARIE  
 TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: USA  
 ZIP: 2202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Tape  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/958,316  
 FILING DATE: 27-OCT-1997  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 94 03179  
 FILING DATE: 18-MAR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 0846-0437-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-1000  
 TELEFAX: (703) 413-2220  
 TELEX: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 145 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-958-316-8

Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.2e-31;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 ELVETRPGDGTFQKWAAYVPSGEQRTCHVQHEGLP 267  
 Db 79 ELVETRPGDGTFQKWAAYVPSGEQRTCHVQHEGLP 117

RESULT 10  
 US-09-949-016-6176  
 Sequence 6176, Application US/09949016  
 Patent No. 6812339

GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 6176  
 LENGTH: 338  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016-6176

Query Match  
 Best Local Similarity 100.0%; Pred. No. 1.8e-30;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 ELVETRPGDGTFQKWAAYVPSGEQRTCHVQHEGLP 267  
 Db 253 ELVETRPGDGTFQKWAAYVPSGEQRTCHVQHEGLP 291

RESULT 11  
 US-09-949-016-8636  
 Sequence 8636, Application US/09949016  
 Patent No. 6812339

GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 20/012  
 SEQ ID NO: 8636  
 LENGTH: 339  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016-8636

Query Match 14.2%; Score 39; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 1.0e-30;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 229 ELVTRPAGDTFQKWAAYVPSGEEQRTCHVQHEGLP 267  
 Db 254 ELVTRPAGDTFQKWAAYVPSGEEQRTCHVQHEGLP 292

RESULT 12  
 US-08-484-905-79  
 Sequence '79, Application US/08484905  
 Patent No. 5976551  
 GENERAL INFORMATION:  
 APPLICANT: Mottez, Estelle  
 ABSTRACTADO, Jean-Pierre  
 APPLICANT: Kourilsky, Philippe  
 TITLE OF INVENTION: An Altered Major Histocompatibility Complex (MHC) Determinant and Methods for Using the Determinant  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finnegan, Henderson, Parabow, Garrett & Dunner  
 STREET: 1300 I Street, N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20005-3315

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy Disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/484,905  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIORITY NUMBER: US 07/792,473  
 FILING DATE: 15-NOV-1991  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25.146  
 REFERENCE/DOCKET NUMBER: 03495.0106-04000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 79:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 289 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-484-905B-79

Query Match 10.9%; Score 30; DB 3; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-21;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 226 QDTELVETPAGDTFQKWAAYVPSGEHQ 255  
 Db 226 QDTELVETPAGDTFQKWAAYVPSGEHQ 255

RESULT 13  
 US-08-481-985B-79  
 Sequence '79, Application US/08481985B  
 Patent No. 601146  
 GENERAL INFORMATION:  
 APPLICANT: Mottez, Estelle  
 ABSTRACTADO, Jean-Pierre  
 APPLICANT: Kourilsky, Philippe  
 TITLE OF INVENTION: Altered Major Histocompatibility Complex  
 NUMBER OF SEQUENCES: 148  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finnegan, Henderson, Parabow, Garrett & Dunner  
 STREET: 1300 I Street, N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/481,985B  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIORITY NUMBER: US 07/792,473  
 FILING DATE: 15-NOV-1991  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25.146  
 REFERENCE/DOCKET NUMBER: 03495.0106-04000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 79:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 289 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-481-985B-79

RESULT 14  
 US-08-370-476-79  
 Sequence '79, Application US/08370476  
 Patent No. 6153408  
 GENERAL INFORMATION:  
 APPLICANT: Mottez, Estelle  
 ABSTRACTADO, Jean-Pierre  
 APPLICANT: Kourilsky, Philippe  
 APPLICANT: Kourilsky, Philippe

Query Match 10.9%; Score 30; DB 2; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-21;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 226 QDTELVETPAGDTFQKWAAYVPSGEHQ 255  
 Db 226 QDTELVETPAGDTFQKWAAYVPSGEHQ 255

APPLICANT: Lone, Yu-Chun  
 APPLICANT: Ojcius, David  
 APPLICANT: Casrouge, Armande  
 TITLE OF INVENTION: Altered Major Histocompatibility Complex  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &  
 ADDRESS: Danner  
 STREET: 1300 I Street, N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20005-3315

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/370,476

FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/117,575  
 FILING DATE: 07-SEP-1993  
 APPLICATION NUMBER: US 08/072,787  
 FILING DATE: 06-JUN-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/801,818  
 FILING DATE: 05-DEC-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/792,473  
 FILING DATE: 15-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REFERENCE DOCKET NUMBER: 25-146  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 79:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 289 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide

US-08-370-476-79

CITY: Washington  
 STATE: D.C.  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy Disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/484,905  
 FILING DATE: 07-JUNE-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/801,818  
 FILING DATE: 05-DEC-1991  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Potter, Jane E. R.  
 REGISTRATION NUMBER: 33,332  
 REFERENCE/DOCKET NUMBER: 03495.0106-03000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 105:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 274 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide

US-08-484-905-105

Query Match Score 10.6%; Score 29; DB 2; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-20;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQDTTELVEVRPAGDGTQFKWAAYVVPSPG 252  
 Db 224 QTQDTTELVEVRPAGDGTQFKWAAYVVPSPG 252

Search completed: July 13, 2005, 09:29:09  
 Job time : 22.8528 secs

RESULT 15  
 US-08-484-905-105  
 Sequence 105, Application US/08484905  
 Patent No. 5976551  
 GENERAL INFORMATION:  
 APPLICANT: Mottez, Estelle  
 APPLICANT: Abastado, Jean-Pierre  
 APPLICANT: Kourilsky, Philippe  
 TITLE OF INVENTION: An Altered Major Histocompatibility Complex (MHC) Determinant and Methods for Using the  
 TITLE OF INVENTION: Determinant  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &  
 ADDRESS: Danner  
 STREET: 1300 I Street, N.W., Suite 700

Result No.	Score	Query Match	Length	DB ID	Description
1	261	72.1	362	A60384	MHC class I histoc
2	113	31.2	345	S07114	MHC class I histoc
3	73	20.2	316	C37028	MHC class I histoc
4	59	16.3	348	S29990	hiscopatibility
5	44	12.2	275	HLHUI0	MHC class I histoc
6	44	12.2	244	S44994	class I histocompa
7	44	12.2	313	I36958	MHC ChIA chain - C
8	44	12.2	154449		MHC class I HLA-CX
9	44	12.2	325	S06424	MHC class I histoc
10	44	12.2	345	I68749	MHC class I lympho
11	44	12.2	354	I54551	hiscopatibility
12	44	12.2	357	I36966	MHC class I protei
13	44	12.2	357	I36966	MHC class I protei
14	44	12.2	359	IHLHUI2	MHC class I histoc
15	44	12.2	364	S03535	class I histocompa
16	44	12.2	365	S01171	class I histocompa
17	44	12.2	365	I36961	MHC class I protei
18	44	12.2	365	I37476	MHC class I histoc
19	44	12.2	365	A47636	MHC class I histoc
20	44	12.2	365	I83063	A11.2 - human
21	44	12.2	365	I56039	HLA-A30.3 precurso
22	44	12.2	365	I61856	MHC class I histoc
23	44	12.2	365	I37478	MHC class I histoc
24	44	12.2	365	I54493	MHC class I histoc
25	44	12.2	365	S77963	MHC class I histoc
26	44	12.2	365	I38519	HLA-AW24 protein
27	44	12.2	365	I54416	HLA-A-0102 allele
28	44	12.2	365	I38518	MHC class I histoc
29	44	12.2	366	IHLHUN3	

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	MHC class I histoc	30	44	12.2	366	2	I37526
OM protein - protein search, using sw model		class I histocoma	31	44	12.2	366	2	JS0262
Run on:	July 13, 2005, 09:02:43 ; Search time 40 Seconds (without alignments)	lymphocyte antigen	32	44	12.2	366	2	I81242
Title:	US-09-819-371-4	MHC class I histoc	33	44	12.2	366	2	I38505
Perfect score:	362	lymphocyte antigen	34	44	12.2	366	2	I37544
Sequence:	1 MAPRSLLLSSGALALATDTW.....QAAVTDSAQSGSVSLTANKV 362	MHC class I histoc	35	44	12.2	366	2	I81241
Scoring table:	OLIGO	MHC HLA-Cw2.2 chai	36	44	12.2	366	2	JH0526
Searched:	283416 seqs, 96216763 residues	MHC class I histoc	37	44	12.2	366	2	I61866
Word size :	0	MHC class I histoc	38	44	12.2	366	2	I37543
Total number of hits satisfying chosen parameters:	283416	MHC class I histocompa	39	44	12.2	366	2	I72113
Minimum DB seq length: 0		MHC class I histoc	40	44	12.2	366	2	I68712
Maximum DB seq length: 2000000000		lymphocyte antigen	41	44	12.2	366	2	S42813
Post-processing: Listing first 45 summaries		MHC class I histoc	42	44	12.2	366	2	B37038
Database :	PIR_79;*	MHC gene HLA-F is expressed in lymphocyte .	43	44	12.2	366	2	I38507
	1: PIR;*	A;Reference number: A60384; PMID:9197889; MUID:9011605; PMID:1707659	44	44	12.2	366	2	I37527
	2: PIR2;*	A;Accession: A60384	45	44	12.2	366	2	I37135
	3: PIR3;*	A;Molecule type: DNA						
	4: PIR4;*	A;Residues: 1-362 <LUR>						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		A;Cross-references: UNIPROT:P30511						
		R;Geraghty, D.B.; Wei, X.; Orr, H.T.; Koller, B.H.						
		C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004						
		C;Accession: A60384; JU0147						
		R;Lury, D.; Epstein, H.; Holmes, N.						
		J. Exp. Med. 171, 1-18, 1990						
		A;Title: Human leukocyte antigen F (HLA-F); an expressed HLA gene composed of a class I						
		A;Reference number: A60384; PMID:9197889; MUID:9011605; PMID:1707659						
		A;Accession: JU0147						
		A;Molecule type: DNA						
		A;Cross-references: GB:X17093; NID:G32223; PIDN:CAA34947.1; PID:g312407						
		A;Cross-references: lymphoblastoid cell line						
		C;Experimental source: lymphoblastoid cell line						
		C;Genetics:						
		A;Gene: GDB:HLA-F						
		A;Cross-references: GDB:125714						
		A;Map position: 6p21.3-6p21.3						
		A;Introns: 22/1; 112/1; 346/1; 366/1; 335/1; 346/1; 366/1						
		C;Superfamily: class I histocompatibility antigen; immunoglobulin homology						
		C;Keywords: glycoprotein; heterodimer; transmembrane protein						
		F;1-21/Domain: signal sequence #status predicted <SIG>						
		F;22-11/Domain: alpha-1 <Al1>						
		F;78-10/Region: hypervariable						
		F;112-23/Domain: alpha-2 <Al2>						
		F;64-192/Region: hypervariable						
		F;204-25/Domain: alpha-3 <Al3>						
		F;217-232/Domain: immunoglobulin homology <IMM>						
		F;107/Binding site: carbohydrate (Asn) (covalent) #status predicted						
Query Match	72.1%	Score 261; DB 2; Length 362;						
Best Local Similarity	99.7%	Pred. No. 8.1e-249;						
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;								
QY	1	MAPRLILLLSGALALTDTWGSHSLRFSTAVSRPGRGPRTAVVEYDDTOPFLRFDS	60					
Db	1	MAPRLILLLSGALALTDTWGSHSLRFSTAVSRPGRGPRTAVVEYDDTOPFLRFDS	60					
QY	61	AAFRMEEPREPWWYEQGQWYETGTAKANAOQTDRVALNLRLRYNOSEAGHTLQGMN	120					
Db	61	AAFRMEEPREPWWYEQGQWYETGTAKANAOQTDRVALNLRLRYNOSEAGHTLQGMN	120					
QY	121	GCDNGPDGRLLRGYTHOAYDGKDYISLNEDLSRWTAAADTVQITQRFYEAEEFPRY	180					

Sequence Comparison Results									
Query Sequence		Target Sequence		Match Statistics		Similarity		Homology	
Db	121	GCDMPGPPGRLLRGYHQAQDGYDQYDLYSNEEDRSWTAADTVQITQRFYAEAEFRY	180	Query Match Score: 20.2%; Best Local Similarity: 100.0%; Matches: 73; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;		Score: 73; DB: 2; Length: 316;			
Db	181	LEGECLLRLRLRLQLRQADPKXAHVAAHPISSHEATRCWALGYDAEITLTWQR	240	Qy	216	SDHEATLRCWALGYPAEITLTWORDGEETQDTTELVTTRPAGDTFQKWAAYVPSGES	275	Qy	SDHEATLRCWALGYPAEITLTWORDGEETQDTTELVTTRPAGDTFQKWAAYVPSGES 228
Db	181	LEGECLLRLRLRLQLRQADPKXAHVAAHPISSHEATRCWALGYDAEITLTWQR	240	Db	169	SDHEATLRCWALGYPAEITLTWORDGEETQDTTELVTTRPAGDTFQKWAAYVPSGES	275	Db	SDHEATLRCWALGYPAEITLTWORDGEETQDTTELVTTRPAGDTFQKWAAYVPSGES 228
Qy	241	DGEHQQTQDTTELVTTRPAGDTFQKWAAYVPSGEETCYHQEGLPQPPLLRWQSPQ	300	Qy	276	QRYTCVHQEGLP	288	Qy	QRYTCVHQEGLP 288
Db	241	DGEHQQTQDTTELVTTRPAGDTFQKWAAYVPSGEETCYHQEGLPQPPLLRWQSPQ	300	Db	229	QRYTCVHQEGLP	241	Db	QRYTCVHQEGLP 241
Qy	301	PPIPIVGIVAGLVLGAVVTTGAVVAAMWRKSSDANGYSQSANTDSAGSGVSILAN	360	RESULT 4	S29990	histocompatibility antigen, HLA-P-like - rhesus macaque			
Qy	301	PPIPIVGIVAGLVLGAVVTTGAVVAAMWRKSSDANGYSQSANTDSAGSGVSILAN	360	C;Species: Macaca mulatta (rhesus macaque)					
Db	361	KV 362	Db	C;Accession: S29995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004					
Qy	361	KV 362	Db	C;Accession: S29990 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004					
Qy	361	KV 362	Db	R;Bontron, R.R.					
Qy	361	KV 362	Db	submitted to the EMBL Data Library, February 1993					
Qy	361	KV 362	Db	A;Reference number: S29990					
Qy	361	KV 362	Db	A;Status: preliminary					
Qy	361	KV 362	Db	A;Molecule type: mRNA					
Qy	361	KV 362	Db	A;Cross-references: UNIPROT:P33617; EMBL:Z21819; NID:938568; PID:CAA79885_1; PMID:938569					
Qy	361	KV 362	Db	C;Superfamily: class I histocompatibility antigen; immunoglobulin homology					
Qy	361	KV 362	Db	C;Keywords: transmembrane protein					
Qy	361	KV 362	Db	F;219-284/Domain: immunoglobulin homology <IMM>					
Qy	361	KV 362	Db	Query Match Score: 16.3%; Best Local Similarity: 100.0%; Matches: 59; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;					
Qy	361	KV 362	Db	Score: 59; DB: 2; Length: 348;					
Qy	361	KV 362	Db	A;Status: preliminary					
Qy	361	KV 362	Db	A;Molecule type: mRNA					
Qy	361	KV 362	Db	A;Residues: 1-345 <LW>					
Qy	361	KV 362	Db	C;Superfamily: class I histocompatibility antigen; immunoglobulin homology <IMM>					
Qy	361	KV 362	Db	C;Keywords: glycoprotein; membrane protein					
Qy	361	KV 362	Db	F;217-282/Domain: immunoglobulin homology <IMM>					
Qy	361	KV 362	Db	Query Match Score: 31.2%; Best Local Similarity: 100.0%; Matches: 113; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;					
Qy	361	KV 362	Db	Score: 113; DB: 2; Length: 345;					
Qy	361	KV 362	Db	A;Status: preliminary					
Qy	361	KV 362	Db	A;Molecule type: mRNA					
Qy	361	KV 362	Db	A;Residues: 1-345 <LW>					
Qy	361	KV 362	Db	C;Species: Homo sapiens (man)					
Qy	361	KV 362	Db	C;Cross-references: UNIPROT:P01892; GB:M11887; NID:9184157; PID:9184158					
Qy	361	KV 362	Db	C;Genetics:					
Qy	361	KV 362	Db	A;Gene: GBP:HLA-A					
Qy	361	KV 362	Db	A;Cross-references: GDB:119310; OMIM:142800					
Qy	361	KV 362	Db	A;Map position: 6p21.3-6p1.3					
Qy	361	KV 362	Db	C;Superfamily: class I histocompatibility antigen; immunoglobulin homology					
Qy	361	KV 362	Db	C;Keywords: glycoprotein; heterodimer; transmembrane protein					
Qy	361	KV 362	Db	F;130-195/Domain: immunoglobulin homology <IMM>					
Qy	361	KV 362	Db	F;20/Binding site: carbohydrate (Aan) (covalent)					
Qy	361	KV 362	Db	Query Match Score: 12.2%; Best Local Similarity: 100.0%; Matches: 44; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;					
Qy	361	KV 362	Db	Score: 44; DB: 1; Length: 275;					
Qy	361	KV 362	Db	A;Status: preliminary					
Qy	361	KV 362	Db	A;Molecule type: DNA					
Qy	361	KV 362	Db	A;Residues: 1-275 <DVAR>					
Qy	361	KV 362	Db	A;Cross-references: UNIPROT:P01892; GB:M11887; NID:9184157; PID:9184158					
Qy	361	KV 362	Db	C;Genetics:					
Qy	361	KV 362	Db	A;Gene: GBP:HLA-C					
Qy	361	KV 362	Db	A;Cross-references: GDB:119311; OMIM:142840					
Qy	361	KV 362	Db	A;Map position: 6p21.3-6p21.3					
Qy	361	KV 362	Db	C;Superfamily: class I histocompatibility antigen; immunoglobulin homology					
Qy	361	KV 362	Db	F;170-235/Domain: immunoglobulin homology <IMM>					
Qy	361	KV 362	Db	Query Match Score: 12.2%; Best Local Similarity: 100.0%; Matches: 44; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;					
Qy	361	KV 362	Db	Score: 44; DB: 1; Length: 275;					
Qy	361	KV 362	Db	A;Status: preliminary					
Qy	361	KV 362	Db	A;Molecule type: DNA					
Qy	361	KV 362	Db	A;Residues: 1-275 <CTA>					
Qy	361	KV 362	Db	A;Cross-references: UNIPROT:Q96FQ5; UNIPROT:Q9MM34; UNIPROT:O19677; UNIF					
Qy	361	KV 362	Db	C;Species: Homo sapiens (man)					
Qy	361	KV 362	Db	C;Cross-references: GDB:119308; OMIM:142800					
Qy	361	KV 362	Db	A;Map position: 6p21.3-6p1.3					
Qy	361	KV 362	Db	C;Superfamily: class I histocompatibility antigen; immunoglobulin homology					
Qy	361	KV 362	Db	C;Keywords: glycoprotein; heterodimer; transmembrane protein					
Qy	361	KV 362	Db	F;130-195/Domain: immunoglobulin homology <IMM>					
Qy	361	KV 362	Db	F;20/Binding site: carbohydrate (Aan) (covalent)					
Qy	361	KV 362	Db	Query Match Score: 12.2%; Best Local Similarity: 100.0%; Matches: 44; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;					
Qy	361	KV 362	Db	Score: 44; DB: 1; Length: 275;					
Qy	361	KV 362	Db	A;Status: preliminary					
Qy	361	KV 362	Db	A;Molecule type: DNA					
Qy	361	KV 362	Db	A;Residues: 1-275 <CTA>					
Qy	361	KV 362	Db	A;Cross-references: UNIPROT:Q96FQ5; UNIPROT:Q9MM34; UNIPROT:O19677; UNIF					
Qy	361	KV 362	Db	C;Species: Homo sapiens (man)					
Qy	361	KV 362	Db	C;Cross-references: GDB:119311; OMIM:142840					
Qy	361	KV 362	Db	A;Map position: 6p21.3-6p21.3					
Qy	361	KV 362	Db	C;Superfamily: class I histocompatibility antigen; immunoglobulin homology					
Qy	361	KV 362	Db	C;Keywords: glycoprotein; heterodimer; transmembrane protein					
Qy	361	KV 362	Db	F;130-195/Domain: immunoglobulin homology <IMM>					
Qy	361	KV 362	Db	F;20/Binding site: carbohydrate (Aan) (covalent)					
Qy	361	KV 362	Db	Query Match Score: 12.2%; Best Local Similarity: 100.0%; Matches: 44; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;					
Qy	361	KV 362	Db	Score: 44; DB: 1; Length: 275;					
Qy	361	KV 362	Db	A;Status: preliminary					
Qy	361	KV 362	Db	A;Molecule type: DNA					
Qy	361	KV 362	Db	A;Residues: 1-275 <CTA>					
Qy	361	KV 362	Db	A;Cross-references: UNIPROT:Q96FQ5; UNIPROT:Q9MM34; UNIPROT:O19677; UNIF					
Qy	361	KV 362	Db	C;Species: Homo sapiens (man)					
Qy	361	KV 362	Db	C;Cross-references: GDB:119311; OMIM:142840					
Qy	361	KV 362	Db	A;Map position: 6p21.3-6p21.3					
Qy	361	KV 362	Db	C;Superfamily: class I histocompatibility antigen; immunoglobulin homology					
Qy	361	KV 362	Db	C;Keywords: glycoprotein; heterodimer; transmembrane protein					
Qy	361	KV 362	Db	F;130-195/Domain: immunoglobulin homology <IMM>					
Qy	361	KV 362	Db	F;20/Binding site: carbohydrate (Aan) (covalent)					
Qy	361	KV 362	Db	Query Match Score: 12.2%; Best Local Similarity: 100.0%; Matches: 44; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;					
Qy	361	KV 362	Db	Score: 44; DB: 1; Length: 275;					
Qy	361	KV 362	Db	A;Status: preliminary					
Qy	361	KV 362	Db	A;Molecule type: DNA					
Qy	361	KV 362	Db	A;Residues: 1-275 <CTA>					
Qy	361	KV 362	Db	A;Cross-references: UNIPROT:Q96FQ5; UNIPROT:Q9MM34; UNIPROT:O19677; UNIF					
Qy	361	KV 362	Db	C;Species: Homo sapiens (man)					
Qy	361	KV 362	Db	C;Cross-references: GDB:119311; OMIM:142840					
Qy	361	KV 362	Db	A;Map position: 6p21.3-6p21.3					
Qy	361	KV 362	Db	C;Superfamily: class I histocompatibility antigen; immunoglobulin homology					
Qy	361	KV 362	Db	C;Keywords: glycoprotein; heterodimer; transmembrane protein					
Qy	361	KV 362	Db	F;130-195/Domain: immunoglobulin homology <IMM>					
Qy	361	KV 362	Db	F;20/Binding site: carbohydrate (Aan) (covalent)					
Qy	361	KV 362	Db	Query Match Score: 12.2%; Best Local Similarity: 100.0%; Matches: 44; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;					
Qy	361	KV 362	Db	Score: 44; DB: 1; Length: 275;					
Qy	361	KV 362	Db	A;Status: preliminary					
Qy	361	KV 362	Db	A;Molecule type: DNA					
Qy	361	KV 362	Db	A;Residues: 1-275 <CTA>					
Qy	361	KV 362	Db	A;Cross-references: UNIPROT:Q96FQ5; UNIPROT:Q9MM34; UNIPROT:O19677; UNIF					
Qy	361	KV 362	Db	C;Species: Homo sapiens (man)					
Qy	361	KV 362	Db	C;Cross-references: GDB:119311; OMIM:142840					
Qy	361	KV 362	Db	A;Map position: 6p21.3-6p21.3					
Qy	361	KV 362	Db	C;Superfamily: class I histocompatibility antigen; immunoglobulin homology					
Qy	361	KV 362	Db	C;Keywords: glycoprotein; heterodimer; transmembrane protein					
Qy	361	KV 362	Db	F;130-195/Domain: immunoglobulin homology <IMM>					
Qy	361	KV 362	Db	F;20/Binding site: carbohydrate (Aan) (covalent)					
Qy	361	KV 362	Db	Query Match Score: 12.2%; Best Local Similarity: 100.0%; Matches: 44; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;					
Qy	361	KV 362	Db	Score: 44; DB: 1; Length: 275;					
Qy	361	KV 362	Db	A;Status: preliminary					
Qy	361	KV 362	Db	A;Molecule type: DNA					
Qy	361	KV 362	Db	A;Residues: 1-275 <CTA>					
Qy	361	KV 362	Db	A;Cross-references: UNIPROT:Q96FQ5; UNIPROT:Q9MM34; UNIPROT:O19677; UNIF					
Qy	361	KV 362	Db	C;Species: Homo sapiens (man)					
Qy	361	KV 362	Db	C;Cross-references: GDB:119311; OMIM:142840					
Qy	361	KV 362	Db	A;Map position: 6p21.3-6p21.3					
Qy	361	KV 362	Db	C;Superfamily: class I histocompatibility antigen; immunoglobulin homology					
Qy	361	KV 362	Db	C;Keywords: glycoprotein; heterodimer; transmembrane protein					
Qy	361	KV 362	Db	F;130-195/Domain: immunoglobulin homology <IMM>					
Qy	361	KV 362	Db	F;20/Binding site: carbohydrate (Aan) (covalent)					
Qy	361	KV 362	Db	Query Match Score: 12.2%; Best Local Similarity: 100.0%; Matches: 44; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;					
Qy	361	KV 362	Db	Score: 44; DB: 1; Length: 275;					
Qy	361	KV 362	Db	A;Status: preliminary					
Qy	361	KV 362	Db	A;Molecule type: DNA					
Qy	361	KV 362	Db	A;Residues: 1-275 <CTA>					
Qy	361	KV 362	Db	A;Cross-references: UNIPROT:Q96FQ5; UNIPROT:Q9MM34; UNIPROT:O19677; UNIF					
Qy	361	KV 362	Db	C;Species: Homo sapiens (man)					
Qy	361	KV 362	Db	C;Cross-references: GDB:119311; OMIM:142840					
Qy	361	KV 362	Db	A;Map position: 6p21.3-6p21.3					
Qy	361	KV 362	Db	C;Superfamily: class I histocompatibility antigen; immunoglobulin homology					
Qy	361	KV 362	Db	C;Keywords: glycoprotein; heterodimer; transmembrane protein					
Qy	361	KV 362	Db	F;130-195/Domain: immunoglobulin homology <IMM>					
Qy	361	KV 362	Db	F;20/Binding site: carbohydrate (Aan) (covalent)				</	

S44994 Class I histocompatibility antigen HLA-Cw6 precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004

C:Accession: S44994 R:Marget, M.; Brockstedt, D.; Jenisch, S.

Submitted to the EMBL Data Library, May 1994

A:Description: New HLA-Cw6 sequence.

A:Reference number: S44994

A:Molecule type: mRNA

A:Residues: 1-98 <MAR>

A:Cross-references: UNIPROT:Q29866; EMBL:233459; PIDN:CA83881.1; PID:94883

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

F:1-72/Domain: signal sequence #status predicted <SIG>

P:1-23-285/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 100.0%; Pred. No. 3.8e-35; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 245 QTQTELVETRPAAGDTFQKWAAYVPSGEQEYRTCHYQHEGLP 288

Db 248 QTQTELVETRPAAGDTFQKWAAYVPSGEQEYRTCHYQHEGLP 291

RESULT 7

136958 HMC Ch1a chain - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C:Accession: 136958

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-313 <RES>

A:Cross-references: UNIPROT:Q30989; GB:M21046; PIDN:AAA35425.1; PID:9176817

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology <IMM>

F:167-232/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 100.0%; Pred. No. 4e-35; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 245 QTQTELVETRPAAGDTFQKWAAYVPSGEQEYRTCHYQHEGLP 288

Db 195 QTQTELVETRPAAGDTFQKWAAYVPSGEQEYRTCHYQHEGLP 238

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology F:179-244/Domain: immunoglobulin homology

Query Match Best Local Similarity 100.0%; Pred. No. 4.1e-35; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 QTQTELVETRPAAGDTFQKWAAYVPSGEQEYRTCHYQHEGLP 288

Db 207 QTQTELVETRPAAGDTFQKWAAYVPSGEQEYRTCHYQHEGLP 250

RESULT 9

SD6424 HMC Class I histocompatibility antigen Ch25 alpha chain precursor - chimpanzee

N:Alternative names: HMC Ch1a chain

C:Species: Pan troglodytes (chimpanzee)

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S06124; I36959

R:Lawlor, D.A.; Ward, P.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.

Nature 335, 268-271, 1988

A:Reference number: S06124; MUID:88319000; PMID:3412487

A:Accession: S06424

A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.

A:Reference number: I36956; MUID:89235215; PMID:2715640

A:Accession: I36959

A:Molecule type: mRNA

A:Residues: 1-332 <LAR>

A:Cross-references: UNIPROT:Q30990

R:Parham, P.; Lawlor, D.A.; Loman, C.B.; Ennis, P.D.

J: Immunol. 142, 3937-3950, 1989

A:Title: Diversity and diversification of HLA-A, B, C alleles.

A:Reference number: I36956; MUID:89235215; PMID:2715640

A:Accession: 136958

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-313 <RES>

A:Cross-references: UNIPROT:Q30989; GB:M21046; PIDN:AAA35425.1; PID:9176817

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology <IMM>

F:167-232/Domain: immunoglobulin homology <IMM>

F:220-285/Domain: immunoglobulin homology <IMM>

F:307-331/Domain: transmembrane #status predicted <TM>

F:110/Binding site: carbohydrate #status predicted <Covalent>

F:125-182,227-283/Disulfide bonds: #status predicted

Query Match Best Local Similarity 100.0%; Pred. No. 4.2e-35; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 245 QTQTELVETRPAAGDTFQKWAAYVPSGEQEYRTCHYQHEGLP 288

Db 248 QTQTELVETRPAAGDTFQKWAAYVPSGEQEYRTCHYQHEGLP 291

RESULT 10

I68749 HMC class I lymphocyte antigen - human (fragment)

MHC class I lymphocyte antigen (man)

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004

C:Accession: I68749

R:Pohla, H.; Kwon, W.; Tabaczewski, P.; Doerner, C.; Weiss, B.H.

Immunogenetics 29, 297-307, 1989

A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B

A:Accession number: I54457; MUID:8933295; PMID:2714852

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-345 <RES>

A:Cross-references: UNIPROT:Q29963; GB:M28206; NID:9576476; PIDN:AAA57258.1; PID:957647

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

F:199-264/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 12.2%; Score 44; DB 2; Length 345;

Best Local Similarity 100.0%; Pred. No. 4.3e-35; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A; Reference number: I36965; MUID:93279743; PMID:8505066  
A; Accession: I36965  
A; Status: preliminary; translated from GB/EMBL/DDBJ  
A; Molecule type: mRNA  
A; Residues: 1-357 <RES>  
A; Cross-references: UNIPROT:Q9NXL1; UNIPROT:Q30992; NID:9176834; PIDN:AAA7204  
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology F; 212-277/Domain: immunoglobulin homology <IMM>

**RESULT 11**

154551 Query Match 12.2%; Score 44; DB 2; Length 357; Best Local Similarity 100.0%; Pred. No. 4.5e-35; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C; Species: Macaca fascicularis (crab-eating macaque) (fragment)  
C; Accession: 154551  
C; Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004  
R; Boyson, J.E.; McAdam, S.N.; Gallimore, A.; Golos, T.G.; Liu, X.; Gotch, F.M.; Hughes, Immunogenetics 41, 59-68, 1995  
A; Title: The MHC B locus in macaques is polymorphic and is conserved between macaques and humans  
A; Reference: 154551  
A; Status: preliminary; translated from GB/EMBL/DDBJ  
A; Molecule type: mRNA  
A; Residues: 1-354 <RES>  
A; Cross-references: UNIPROT:Q95513; EMBL:U02976; NID:9413827; PIDN:AAA70050.1; PMID:94138  
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology F; 209-274/Domain: immunoglobulin homology <IMM>

Query Match 12.2%; Score 44; DB 2; Length 354; Best Local Similarity 100.0%; Pred. No. 4.4e-35; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C; Species: Ban troglopytes (chimpanzee) (fragment)  
C; Accession: 136966  
C; Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 09-Jul-2004  
C; Cross-references: UNIPROT:Q9NXL2; UNIPROT:Q30993; NID:9176836; PIDN:AAA0366  
R; Chen, Z.W.; Hughes, A.L.; Ghim, S.H.; Letvin, N.L.; Watkins, D.I.  
Immunogenetics 38, 238-240, 1993  
A; Reference number: 136965; MUID:93279743; PMID:8505066  
A; Accession: 136966  
A; Status: preliminary; translated from GB/EMBL/DDBJ  
A; Molecule type: mRNA  
A; Residues: 1-357 <RES>  
A; Cross-references: UNIPROT:Q9NXL2; UNIPROT:Q30993; GB:M55245; NID:9176836; PIDN:AAA0366  
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology F; 212-277/Domain: immunoglobulin homology <IMM>

Query Match 12.2%; Score 44; DB 2; Length 357; Best Local Similarity 100.0%; Pred. No. 4.5e-35; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C; Species: Pan troglodytes (chimpanzee) (fragment)  
C; Accession: 136965  
C; Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
R; Chen, Z.W.; Hughes, A.L.; Ghim, S.H.; Letvin, N.L.; Watkins, D.I.  
Immunogenetics 38, 238-240, 1993  
A; Title: Two more chimpanzee Patr-A locus alleles related to the HLA-A1/A3/A11 family.

**RESULT 12**

136966 Query Match 12.2%; Score 44; DB 1; Length 359; Best Local Similarity 100.0%; Pred. No. 4.5e-35; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C; Species: Pan troglodytes (chimpanzee) (fragment)  
C; Accession: 136966  
C; Date: 18-Oct-1995 #sequence\_revision 18-Oct-1995 #text\_change 09-Jul-2004  
R; Mayer, W.B.; Jonker, M.; Klein, D.; van Seerten, G.; Klein, J.  
EMBO J., 14, 2765-2774, 1995  
A; Title: Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species recombination  
A; Reference number: S01171; MUID:8930641; PMID:2460344  
A; Molecule type: mRNA  
A; Residues: 1-364 <WAV>  
A; Cross-references: UNIPROT:P13748; EMBL:X13113; NID:938212; PIDN:CAA31505.1; PMID:97557;  
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology

**RESULT 13**

136965 Query Match 12.2%; Score 44; DB 1; Length 359; Best Local Similarity 100.0%; Pred. No. 4.5e-35; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C; Species: Pan troglodytes (chimpanzee) (fragment)  
C; Accession: 136965  
C; Date: 13-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
R; Chen, Z.W.; Hughes, A.L.; Ghim, S.H.; Letvin, N.L.; Watkins, D.I.  
Immunogenetics 38, 238-240, 1993  
A; Title: Two more chimpanzee Patr-A locus alleles related to the HLA-A1/A3/A11 family.

C:Keywords: transmembrane protein  
P:1-23/Domain: signal sequence (fragment) #status predicted <SIG>  
P:24-364/Product: class I histocompatibility antigen alpha chain #status predicted <MAT>  
P:24-297/Domain: extracellular #status predicted <EXT>  
P:219-284/Domain: immunoglobulin homology <IMM>  
P:298-336/Domain: transmembrane #status predicted <TM>  
P:337-364/Domain: intracellular #status predicted <INT>  
  
Query Match 12.2%; Score 44; DB 2; Length 364;  
Best Local Similarity 100.0%; Prod. No. 4.e-35;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 245 QTQTELVERPAGDTFQKWAAVVPPSGBEQRTCHYQHEGLP 288  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 247 QTQTELVERPAGDTFQKWAAVVPPSGBEQRTCHYQHEGLP 290

Search completed: July 13, 2005, 09:15:25  
Job time : 41 secs

**THIS PAGE BLANK (USPTO)**

Gencore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.  
**1 Protein - Protein search, using SW model.**  
 run on: July 13, 2005, 09:25:40 ; Search time 120.47 Seconds  
 (without alignments)  
 878.681 Million cell updates/sec  
 title: US-09-819-371-5  
 perfect score: 274  
 sequence: 1 GSHSLRYFSTAVSRPGRGEP.....QRTYCHVQHEGLPQPILLRW 274  
 scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0  
 searched: 1726220 seqs, 386332138 residues  
 word size : 0  
 total number of hits satisfying chosen parameters:  
 1726220  
 post-processing: Listing first 45 summaries  
 database : Published Applications AA:  
 1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:  
 2: /cgn2\_6/ptodata/1/pubppaa/US06\_PUB.pep:  
 3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:  
 4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:  
 Sequence 835, App  
 Sequence 941, App  
 Sequence 16, Appl  
 Sequence 15, Appl  
 Sequence 3072, A  
 Sequence 72, Appl  
 Sequence 156, App  
 Sequence 3805, A  
 Sequence 5, Appli  
 Sequence 383, App  
 Sequence 1135, Ap  
 Sequence 387, App  
 Sequence 1143, Ap  
 Sequence 8, Appli  
 Sequence 384, App  
 Sequence 1142, Ap  
 Sequence 3648, Ap  
 Sequence 7, Appli  
 Sequence 380, App  
 Sequence 388, App  
 Sequence 1134, Ap  
 Sequence 1139, Ap  
 Sequence 379, App  
 Sequence 1139, Ap  
 Sequence 78, App  
 Sequence 160, App  
 Sequence 8, Appli  
 Sequence 35461, A  
 Sequence 799, App  
 Sequence 2139, App  
 Sequence 2139, App  
 Sequence 2139, App

21 TRANSACTIONS

SUMMARIES						
Query	Match	Length	DB	ID	Description	
cgna_6_ptodata_1_pubcaa_uso0_pubcomb_pep:	10:	274	11	US-09-819-371-5	Sequence 5, Appl	
cgna_6_ptodata_1_pubcaa_uso9b_pubcomb_pep:	11:	362	15	US-10-257-021-82	Sequence 82, Appl	
cgna_6_ptodata_1_pubcaa_uso9c_pubcomb_pep:	12:	442	16	US-10-408-765A-1887	Sequence 1887, Ap	
cgna_6_ptodata_1_pubcaa_uso9_nem_pub_pep:	13:	271	9	US-09-925-301-1431	Sequence 1431, Ap	
cgna_6_ptodata_1_pubcaa_uso10_pubcomb_pep:	14:	362	11	US-09-819-371-4	Sequence 4, Appl	
cgna_6_ptodata_1_pubcaa_uso10b_pubcomb_pep:	15:	215	11	US-09-819-371-6	Sequence 6, Appl	
cgna_6_ptodata_1_pubcaa_uso10c_pubcomb_pep:	16:	386	15	US-10-264-049-1063	Sequence 4063, Ap	
cgna_6_ptodata_1_pubcaa_uso10_pubcomb_pep:	17:	386	15	US-10-029-386-30718	Sequence 30718, A	
cgna_6_ptodata_1_pubcaa_uso10_nem_pub_pep:	18:	77	14	US-10-029-386-34273	Sequence 34273, A	
cgna_6_ptodata_1_pubcaa_uso11_pubcomb_pep:	19:	91	14	US-10-029-386-31089	Sequence 31089, A	
cgna_6_ptodata_1_pubcaa_uso11_new_pub_pep:	20:	274	11	US-09-819-371-5	SEQ ID NO 5	
cgna_6_ptodata_1_pubcaa_uso11_new_pub_pep:	21:	274	11	US-09-819-371-5	TYPE: BRT	
cgna_6_ptodata_1_pubcaa_uso0_pubcomb_pep:	22:	274	11	US-09-819-371-5	ORGANISM: Homo sapiens	

Pred. No. 19 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	274	100.0	274	11	US-09-819-371-5 Sequence 5 , Appli
2	274	100.0	362	15	US-10-257-021-02 Sequence 82 , Appli
3	274	100.0	442	16	US-10-408-765A-1887 Sequence 1887 , Ap
4	241	68.0	271	9	US-09-925-301-1431 Sequence 1431 , Ap
5	175	63.9	362	11	US-09-819-371-4 Sequence 4 , Appli
6	119	43.4	215	11	US-09-819-371-6 Sequence 6 , Appli
7	70	25.5	186	15	US-10-264-049-1063 Sequence 4063 , Ap
8	68	24.8	96	14	US-10-029-386-30718 Sequence 30718 , A
9	44	16.1	77	14	US-10-029-386-34273 Sequence 34273 , A
10	44	16.1	91	14	US-10-029-386-1089 Sequence 31089 , A
11	44	16.1	104	9	US-09-925-302-815 Sequence 835 , Ann

Qy 161 RADPPKAHVAHHPSDHATLRCWALGYPAETITLWQDGEQTOQTELVETRPGDT 240  
 Db 161 RADPPKAHVAHHPSDHATLRCWALGYPAETITLWQDGEQTOQTELVETRPGDT 240  
 Qy 241 FQKWAAYVVPSGEQRYTCHVQHEGLPPLILRW 274  
 Db 241 FQKWAAYVVPSGEQRYTCHVQHEGLPPLILRW 274

## RESULT 2

US-10-257-021-82

; Sequence 82, Application US/10257021  
 ; Publication No. US20030211498A1

; GENERAL INFORMATION

; APPLICANT: Morin, Patrice J.

; Pizer, Eileen S.

; APPLICANT: Hough, Colleen D.

; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER

; FILE REFERENCE: 14014\_036902

; CURRENT APPLICATION NUMBER: US/10/257,021

; CURRENT FILING DATE: 2002-10-03

; PRIOR APPLICATION NUMBER: PCT/US01/10947

; PRIOR FILING DATE: 2001-04-03

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: FastSEQ For Windows Version 4.0

; SEQ ID NO: 82

; LENGTH: 362

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-257-021-82

Query Match 100.0%; Score 274; DB 15; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-60;  
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 1 GSHSLRYFSTAVSRPGRGEPRTIAVEYDDTQFLRFDSAAIPRMPEPREPWEQEGLQYW 60  
 Db 22 GSHSLRYFSTAVSRPGRGEPRTIAVEYDDTQFLRFDSAAIPRMPEPREPWEQEGLQYW 81

Qy 61 EWTGTYAKANAQTDRVALNLRLRYNQSEASHTLQNGMCDGPDRLLRGYHQHYDG 120

Db 82 EWTGTYAKANAQTDRVALNLRLRYNQSEASHTLQNGMCDGPDRLLRGYHQHYDG 141

Qy 121 KDYISLNEDLSRWSATAADTVQAQTDRVALNLRLRYNQSEASHTLQNGMCDGPDRLLRGYHQHYDG 180

Db 142 KDYISLNEDLSRWSATAADTVQAQTDRVALNLRLRYNQSEASHTLQNGMCDGPDRLLRGYHQHYDG 201

Qy 181 RADPKAHVAHHPSDHATLRCWALGYPAETITLWQDGEQTOQTELVETRPGDT 240

Db 202 RADPKAHVAHHPSDHATLRCWALGYPAETITLWQDGEQTOQTELVETRPGDT 261

Qy 241 FQKWAAYVVPSCSEQRVTCHVQHEGLPPLILRW 274

Db 262 FQKWAAYVVPSCSEQRVTCHVQHEGLPPLILRW 295

; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

; FILE REFERENCE: 660088\_465

; CURRENT APPLICATION NUMBER: US/10/408,765A

; CURRENT FILING DATE: 2003-04-04

; NUMBER OF SEQ ID NOS: 3077

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 1887

; LENGTH: 442

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-765A-1887

; Sequence 1887, Application US/10408765A

; Publication No. US20040101874A1

; GENERAL INFORMATION:

; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Fahy, Bojin D.

; APPLICANT: Zhang, Bing

; APPLICANT: Taylor, Steven W.

; APPLICANT: Glenn, Gary M.

; APPLICANT: Warock, Dale E.

; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

Db 148 KDIISLNEDLRSWTAADTVQITQRFYAEFRRTYLEGECLELLRRYLENGKETLQ 207  
 Qy 181 RADPKHAYAHHP1SDHEATLRCWALGFYPAEITLTWQDGBEQTQDTELVERPAGT 240  
 Db 208 RADPKHAYAHHP1SDHEATLRCWALGFYPAEITLTWQDGBEQTQDTELVERPAGT 267

Qy 241 F 241  
 Db 268 F 268

RESULT 5  
 US-09-819-371-4  
 ; Sequence 4, Application US/09819371  
 ; Publication No. US20040053344A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Egawa, Kohji  
 ; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can  
 ; TITLE OF INVENTION: Using Thereof  
 ; FILE REFERENCE: 3.0815  
 ; CURRENT APPLICATION NUMBER: US/09/819,371  
 ; CURRENT FILING DATE: 2002-03-15  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 4  
 ; LENGTH: 362  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-819-371-4

Query Match Score 63.9%; Best Local Similarity 100.0%; Matches 115; Pred. No. 5e-163; Length 362;  
 保守型 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSLRYFSTAVSRPGRGEPRTYAVEYYDDTOFLRFDSDAIPRMEPRPWQEQQPYW 60  
 Db 22 GHSLRYFSTAVSRPGRGEPRTYAVEYYDDTOFLRFDSDAIPRMEPRPWQEQQPYW 81

Qy 61 EWTGYAKANAQTDRVVALNLRLRYNQSEASGHTLQNGANGCDMGPDGHLLRGYTHQHDG 120  
 Db 82 EWTGYAKANAQTDRVVALNLRLRYNQSEASGHTLQNGANGCDMGPDGHLLRGYTHQHDG 141

Qy 121 KDIISLNEDLRSWTAADTVQITQRFYAEFRRTYLEGECLELLRRYLENG 175  
 Db 142 KDIISLNEDLRSWTAADTVQITQRFYAEFRRTYLEGECLELLRRYLENG 196

RESULT 6  
 US-09-819-371-6  
 ; Sequence 6, Application US/09819371  
 ; Publication No. US20040053344A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Egawa, Kohji  
 ; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can  
 ; TITLE OF INVENTION: Using Thereof  
 ; FILE REFERENCE: 3.0815  
 ; CURRENT APPLICATION NUMBER: US/09/819,371  
 ; CURRENT FILING DATE: 2002-03-15  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 6  
 ; LENGTH: 215  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-819-371-6

Query Match Score 43.4%; Best Local Similarity 100.0%; Matches 119; Pred. No. 3e-1e-18; Length 215;  
 保守型 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 DGKDYISLNEDLRSWTAADTVQITQRFYAEFRRTYLEGECLELLRRYLENGKET 178  
 Db 97 DGKDYISLNEDLRSWTAADTVQITQRFYAEFRRTYLEGECLELLRRYLENGKET 156

OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

FEATURE: MISC FEATURE

LOCATION: (180)

OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

US-10-264-09-4063

Query Match 25.5%; Score 70; DB 15; Length 186;

Best Local Similarity 100.0%; Pred. No. 3.5e-60; Indels 0; Gaps 0;

Matches 70; Conservative 0; Mismatches 0; Delins 0; Gaps 0;

Qy 66 YAKANAAQTDRVALRNLLRYNQSEAGSHTLQGMNGCDMGPDRILLRGYHQAYDGDYIS 125

Db 1 YAKANAAQTDRVALRNLLRYNQSEAGSHTLQGMNGCDMGPDRILLRGYHQAYDGDYIS 60

RESULT 8

US-10-029-306-30718

Sequence 30718, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEGOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 30718

LENGTH: 96

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO CHR6.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12

OTHER INFORMATION: SWISSPROT HIT: P30511, EVALU 2.00e-52

US-10-029-306-30718

Query Match 24.8%; Score 68; DB 14; Length 96;

Best Local Similarity 100.0%; Pred. No. 1.8e-38; Indels 0; Gaps 0;

Matches 68; Conservative 0; Mismatches 0; Delins 0; Gaps 0;

Qy 183 DPPKAHVHHPISDHATELRCWALGFPFAEITLTWORDGEQTQDTTELVERTPAGDCTFQ 242

Db 2 DPPKAHVHHPISDHATELRCWALGFPFAEITLTWORDGEQTQDTTELVERTPAGDCTFQ 61

RESULT 9

US-10-029-306-34273

Sequence 34273, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEGOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 34273

LENGTH: 96

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO CHR6.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1

OTHER INFORMATION: SWISSPROT HIT: P30509, EVALU 1.00e-52

US-10-029-306-31099

Query Match 16.1%; Score 44; DB 14; Length 91;

Best Local Similarity 100.0%; Pred. No. 6.3e-35; Indels 0; Gaps 0;

Matches 44; Conservative 0; Mismatches 0; Delins 0; Gaps 0;

Qy 224 QTQDTTELVERTPAGDGTQFMKWAAYVPSGEORYTCHVQHEGLP 267

Db 41 QTQDTTELVERTPAGDGTQFMKWAAYVPSGEORYTCHVQHEGLP 84

RESULT 11

US-09-925-302-835

Sequence 835, Application US/09925302

Patent No. US2004491A1

GENERAL INFORMATION:

APPLICANT: Roben et al.

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

```

: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO: 835
: LENGTH: 104
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE: SITE
: NAME/KEY: SITE
: LOCATION: (95)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835

Query Match          16.1%; Score 44; DB 17; Length 365;
Best Local Similarity 100.0%; Pred. No. 2.e-34;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
: Sequence 16, Application US/10430984
: Publication No. US20040225112A1
: GENERAL INFORMATION:
:   APPLICANT: The Board of Trustees of the University of Arkansas
:   TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)
:   TITLE OF INVENTION: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity
:   FILE REFERENCE: 8793-53098
:   CURRENT APPLICATION NUMBER: US/10/430,984
:   CURRENT FILING DATE: 2003-05-09
:   NUMBER OF SEQ ID NOS: 16
:   SOFTWARE: PatentIn version 3.2
:   SEQ ID NO: 16
:   LENGTH: 476
:   TYPE: PRT
:   ORGANISM: human leukocyte antigen E-Single chain dimer
US-10-430-984-16

Query Match          15.7%; Score 43; DB 16; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
: Sequence 15, Application US/10430984
: Publication No. US20040225112A1
: GENERAL INFORMATION:
:   APPLICANT: Crew, Mark D
:   TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)
:   TITLE OF INVENTION: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity
:   FILE REFERENCE: 8793-53098
:   CURRENT APPLICATION NUMBER: US/10/430,984
:   CURRENT FILING DATE: 2003-05-09
:   NUMBER OF SEQ ID NOS: 16
:   SOFTWARE: PatentIn version 3.2
:   SEQ ID NO: 15
:   LENGTH: 500
:   TYPE: PRT
:   ORGANISM: human leukocyte antigen E-Single chain Trimer
US-10-430-984-15

Query Match          15.7%; Score 43; DB 16; Length 500;
Best Local Similarity 100.0%; Pred. No. 2.7e-33;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
: Sequence 15, Application US/10430984
: Publication No. US20040225112A1
: GENERAL INFORMATION:
:   APPLICANT: CARGILL, Michele et al.
:   TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
:   TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
:   FILE REFERENCE: CL001499
:   CURRENT APPLICATION NUMBER: US/10/741,600
:   CURRENT FILING DATE: 2003-12-22
:   NUMBER OF SEQ ID NOS: 73957
:   SOFTWARE: FastSEQ for Windows Version 4.0
:   SEQ ID NO: 941
:   LENGTH: 365
:   TYPE: PRT
:   ORGANISM: Homo sapiens
US-10-741-600-941

Search completed: July 13, 2005, 09:46:00
Job time : 121.47 secs

```

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 09:09:04 ; Search time 43 Seconds  
 (without alignments)  
 628.441 Million cell updates/sec

Title: US-09-819-371-4

Perfect score: 362

Sequence: 1. MAPRSLLLSGALALTTDTW.....QAAVTDSAQGSVSLTANKV 362

Scoring table: OLTC0 Gap0.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545.

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
 1: /cgpn2\_6/picodata/1/iaa/5A\_COMB.pep.\*  
 2: /cgpn2\_6/picodata/1/iaa/5B\_COMB.pep.\*  
 3: /cgpn2\_6/picodata/1/iaa/6A\_COMB.pep.\*  
 4: /cgpn2\_6/picodata/1/iaa/6B\_COMB.pep.\*  
 5: /cgpn2\_6/picodata/1/iaa/PCUTUS\_COMB.pep.\*  
 6: /cgpn2\_6/picodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	196	54.1	362	4	US-09-949-016-8242	Sequence 8242, AP
2	120	33.1	120	4	US-09-513-999C-4290	Sequence 4290, AP
3	44	12.2	274	1	US-08-22-051-1	Sequence 1, Appl
4	43	11.9	358	4	US-09-949-016-6620	Sequence 6620, AP
5	43	11.9	360	4	US-09-949-016-8370	Sequence 8370, AP
6	39	10.8	117	3	US-08-06-057-9	Sequence 9, Appl
7	39	10.8	117	3	US-08-958-016-9	Sequence 9, Appl
8	39	10.8	145	2	US-08-40-057-8	Sequence 8, Appl
9	39	10.8	145	3	US-08-958-016-8	Sequence 8, Appl
10	39	10.8	338	4	US-09-949-016-6176	Sequence 6176, AP
11	39	10.8	339	4	US-09-949-016-8336	Sequence 8336, AP
12	30	8.3	289	2	US-08-484-005-79	Sequence 79, Appl
13	30	8.3	289	3	US-08-481-985B-79	Sequence 79, Appl
14	30	8.3	289	3	US-08-370-0476-79	Sequence 79, Appl
15	29	8.0	274	2	US-08-484-005-107	Sequence 107, APP
16	29	8.0	274	2	US-08-484-005-107	Sequence 107, APP
17	29	8.0	274	2	US-08-484-005-108	Sequence 108, APP
18	29	8.0	274	3	US-08-481-985B-105	Sequence 107, APP
19	29	8.0	274	3	US-08-481-985B-107	Sequence 107, APP
20	29	8.0	274	3	US-08-481-985B-108	Sequence 108, APP
21	29	8.0	274	3	US-08-370-0476-105	Sequence 105, APP
22	29	8.0	274	3	US-08-370-0476-107	Sequence 107, APP
23	29	8.0	274	3	US-08-370-0476-108	Sequence 108, APP
24	29	8.0	341	3	US-08-89-019-38	Sequence 38, Appl
25	29	8.0	345	2	US-08-484-905-97	Sequence 97, Appl
26	29	8.0	365	2	US-08-484-905-98	Sequence 98, Appl
27	29	8.0	365	2	US-08-484-905-99	Sequence 99, Appl

RESULT 1  
 US-09-949-016-8242  
 ; Sequence 8242, Application US/09949016  
 ; Patent No. 6812339

GENERAL INFORMATION

; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949, 016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 205012  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 8242  
 ; LENGTH: 362  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-09-949-016-8242

Query Match 54.1%; Score 196; DB 4; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-178;  
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPSSLILLSGALALTDTWAGSHSLRYSTAVSRPGRGSPRVTAVYVDDTOFLRFSD 60  
 Db 1 MAPSSLILLSGALALTDTWAGSHSLRYSTAVSRPGRGSPRVTAVYVDDTOFLRFSD 60

Qy 1 AAIRPMERPEPTWQEGPOWYENTGYAKANAQDRAVLNLARYNQSEAGSHTLQGMN 120  
 Db 61 AAIRPMERPEPTWQEGPOWYENTGYAKANAQDRAVLNLARYNQSEAGSHTLQGMN 120

Qy 121 GCDNGPDGRLLRGTHQAYDGKDYLISLNEDLSRWTAAVTQITQRFYEAEYBEFRY 180  
 Db 121 GCDNGPDGRLLRGTHQAYDGKDYLISLNEDLSRWTAAVTQITQRFYEAEYBEFRY 180

RESULT 2  
 US-09-513-999C-4290  
 ; Sequence 4290, Application US/09513999C  
 ; Patent No. 6783361

GENERAL INFORMATION:  
 APPLICANT: Dunas Milne Edwards, J.B.  
 APPLICANT: Duciere, A.  
 APPLICANT: Giordano, J.Y.  
 TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 PATENT NO: 6783961  
 FILE REFERENCE: 59 US2 REG  
 CURRENT APPLICATION NUMBER: US/09/513,999C  
 CURRENT FILING DATE: 2000-05-24  
 PRIOR APPLICATION NUMBER: US 60/122,487  
 PRIOR FILING DATE: 1999-02-26  
 NUMBER OF SEQ ID NOS: 36681  
 SOFTWARE: Patent.pnt  
 SEQ ID NO: 4290  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE: SIGNAL  
 NAME/KEY: SIGNAL  
 LOCATION: -17--1  
 OTHER INFORMATION: score 9.3  
 SEQ ID NO: 513-999C-4290

Query Match      Score 120; DB 4; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-106; Indels 0; Gaps 0;  
 Matches 120; Conservative 0; Mismatches 0;

Qy      1 MAPRLILLLSGALATDTWAGSHSLRYFSTAVSRPGSRGEPRYIAVEYDDTQFLRFDSD 60  
 Db      1 MAPRLILLLSGALATDTWAGSHSLRYFSTAVSRPGSRGEPRYIAVEYDDTQFLRFDSD 60

Qy      61 AAIPRMERPREPWEQEGQWEMTTGAKANQTDYRALNLLRNQSAGSHTLQGMN 120  
 Db      61 AAIPRMERPREPWEQEGQWEMTTGAKANQTDYRALNLLRNQSAGSHTLQGMN 120

---

RESULT 3  
 US-08-222-851-1  
 Sequence 1, Application US/08222851  
 Patent No. 5723128  
 GENERAL INFORMATION:  
 APPLICANT: CLAYBERGER, CAROL A.  
 APPLICANT: KRENICKY, ALAN M.  
 APPLICANT: PARHAM, PETER  
 TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")  
 TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOERSTER  
 STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20006-1812  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/222,851  
 FILING DATE: 05-APR-1994  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MILLMAN, ROBERT A.  
 REGISTRATION NUMBER: 36,217  
 REFERENCE DOCKET NUMBER: 28600-20200.22  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 887-1500  
 TELEFAX: (212) 494-0792  
 TELEX: 90-4030 MRSINFOERSWSH  
 INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 274 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: linear  
 US-08-222-851-1

Query Match      Score 44; DB 1; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-33; Indels 0; Gaps 0;  
 Matches 44; Conservative 0; Mismatches 0;

Qy      245 QTQTELVEVTPAGDTFQRKWAAYVPSGEORYTCVHQHGLP 288  
 Db      224 QTQTELVEVTPAGDTFQRKWAAYVPSGEORYTCVHQHGLP 267

---

RESULT 4  
 US-09-949-016-6620  
 Sequence 6620, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 6620  
 LENGTH: 358  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016-6620

Query Match      Score 43; DB 4; Length 358;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32; Indels 0; Gaps 0;  
 Matches 43; Conservative 0; Mismatches 0;

Qy      246 TQDTTELVEVTPAGDTFQRKWAAYVPSGEORYTCVHQHGLP 288  
 Db      246 TQDTTELVEVTPAGDTFQRKWAAYVPSGEORYTCVHQHGLP 288

---

RESULT 5  
 US-09-949-016-8370  
 Sequence 8370, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 8370  
 LENGTH: 360  
 TYPE: PRT  
 ORGANISM: Human

US-09-949-016-8370  
 Query Match 11.9%; Score 43; DB 4; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 1 6e-32;  
 Matches 43; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 246 TQDTELVTRPAGDTFQKWAAYVPSGEQRYTCVHQHEGLP 288  
 Db 248 TQDTELVTRPAGDTFQKWAAYVPSGEQRYTCVHQHEGLP 290

RESULT 6  
 US-08-406-057-9  
 ; Sequence 9, Application US/08406057  
 ; Patent No. 585642  
 GENERAL INFORMATION:  
 ; APPLICANT: CAROSELLA, EDGARDO D  
 ; APPLICANT: MOREAU, PHILIPPE  
 ; APPLICANT: GLUCKMAN, ELINE  
 ; APPLICANT: KIRSZENBAUM, MAREK  
 ; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
 ; CITY: ARLINGTON  
 ; STATE: VIRGINIA  
 ; COUNTRY: USA  
 ; ZIP: 22022  
 COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Tape  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/958,316  
 ; APPLICATION NUMBER: US/08/958,316  
 ; FILING DATE: 27-OCT-1997  
 ; CLASSIFICATION: 530  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 94 03179  
 ; FILING DATE: 18-MAR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: OBLON, NORMAN F  
 ; REGISTRATION NUMBER: 24,618  
 ; REFERENCE/DOCKET NUMBER: 0846-0437-0  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 413-3000  
 ; TELEFAX: (703) 413-2220  
 ; TELEX: 248855 OPAT UR  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 117 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-958-316-9

Query Match 10.8%; Score 39; DB 3; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 3 5e-29;  
 Matches 39; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 250 ELVETRPAAGDTFQKWAAYVPSGEQRYTCVHQHEGLP 288  
 Db 251 ELVETRPAAGDTFQKWAAYVPSGEQRYTCVHQHEGLP 89

RESULT 8  
 US-08-406-057-8  
 ; Sequence 8, Application US/08406057  
 ; Patent No. 585642  
 GENERAL INFORMATION:  
 ; APPLICANT: CAROSELLA, EDGARDO D  
 ; APPLICANT: MOREAU, PHILIPPE  
 ; APPLICANT: GLUCKMAN, ELINE  
 ; APPLICANT: KIRSZENBAUM, MAREK  
 ; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
 ; CITY: ARLINGTON  
 ; STATE: VIRGINIA  
 ; COUNTRY: USA  
 ; ZIP: 22022  
 COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Tape

RESULT 7  
 US-08-958-316-9  
 ; Sequence 9, Application US/08958316  
 ; Patent No. 6291659  
 ; GENERAL INFORMATION:

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/406,057  
 FILING DATE: 17-MAR-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 94 03179  
 FILING DATE: 18-MAR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F  
 REFERENCE/DOCKET NUMBER: 846-331-0  
 REGISTRATION NUMBER: 24,618  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEFAX: (703) 413-2220  
 TELEX: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 145 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-406-057-8

RESULT 9  
 US-08-958-316-8  
 Sequence 8, Application US/0858316  
 Patent No. 6291659  
 GENERAL INFORMATION:  
 APPLICANT: CAROSSILLA, EDGARDO D  
 APPLICANT: MOREAU, PHILIPPE  
 APPLICANT: GLUCKMAN, ELINNE  
 APPLICANT: KIRSZENBAUM, MARIE  
 TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
 TITLE OF INVENTION: GENE AND THEIR APPLICATIONS  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT  
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: USA  
 ZIP: 22202

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Tape  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/958,316  
 FILING DATE: 27-OCT-1997  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 94 03179  
 FILING DATE: 18-MAR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F  
 REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 0846-0437-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220  
 TELEX: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 145 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-958-316-8

Query Match 10.8%; Score 39; DB 3; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-29;  
 Matches 39; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 250 ELVETRPGDGTFQKWAAYVPSGEQRTCHVQHGLP 288  
 Db 79 ELVETRPGDGTFQKWAAYVPSGEQRTCHVQHGLP 117

RESULT 10  
 US-09-949-016-6176  
 Sequence 6176, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001307  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 6176  
 LENGTH: 338  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016-6176

Query Match 10.8%; Score 39; DB 4; Length 338;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-29;  
 Matches 39; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 250 ELVETRPGDGTFQKWAAYVPSGEQRTCHVQHGLP 288  
 Db 253 ELVETRPGDGTFQKWAAYVPSGEQRTCHVQHGLP 291

RESULT 11  
 US-09-949-016-8636  
 Sequence 8636, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001307  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 8636  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-8636

Query Match 10.8%; Score: 39; DB 4; Length: 339;  
Best Local Similarity 100.0%; Pred. No. 9.7e-29;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 ELVETRPGDGTFOKWAAVVPSGEQRYTCYHVGELP 288  
Db 254 ELVETRPGDGTFOKWAAVVPSGEQRYTCYHVGELP 292

RESULT 12  
US-08-484-905-79  
Sequence '79, Application US/08484905  
GENERAL INFORMATION:  
APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Phillipine  
TITLE OF INVENTION: An Altered Major Histocompatibility Complex  
TITLE OF INVENTION: Determinant and Methods for Using the  
TITLE OF INVENTION: Complex (MHC) Determinant  
NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finegan, Henderson, Parabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,905  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 530

APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-481-985B-79

Query Match 8.3%; Score: 30; DB 3; Length: 289;  
Best Local Similarity 100.0%; Pred. No. 2.9e-20;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 QDTTELVERTPADGDTFOKWAAVVPSGEHQ 276  
Db 226 QDTTELVERTPADGDTFOKWAAVVPSGEHQ 255

RESULT 14  
US-08-370-476-79  
Sequence '79, Application US/08370476  
Patent No. 6153408  
GENERAL INFORMATION:  
APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Phillipine  
APPLICANT: Ocius, David  
APPLICANT: Castouge, Armando  
TITLE OF INVENTION: Altered Major Histocompatibility Complex

SEQ ID NO: 8636  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-8636

Query Match 10.8%; Score: 39; DB 4; Length: 339;  
Best Local Similarity 100.0%; Pred. No. 9.7e-29;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 QDTTELVERTPADGDTFOKWAAVVPSGEHQ 276  
Db 226 QDTTELVERTPADGDTFOKWAAVVPSGEHQ 255

TITLE OF INVENTION:  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 ADDRESSEE: Dunner  
 STREET: 1300 I Street, N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20005-3315

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/370, 476  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/117, 575  
 FILING DATE: 07-SEP-1993  
 APPLICATION NUMBER: US 08/072, 787  
 FILING DATE: 06-JUN-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/801, 818  
 FILING DATE: 05-DEC-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/792, 473  
 FILING DATE: 15-NOV-1991  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 05243.0001-01000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 79:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 289 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-08-370-476-79

Query Match 8.3%; Score 30; DB 3; Length 289;

Best Local Similarity 100.0%; Pred. No. 2.9e-20;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 QDTELVERPAGDTFQRKWAAYVPSGEHQ 276  
 Db 226 QDTELVERPAGDTFQRKWAAYVPSGEQ 255

RESULT 15

US-08-484-905-105

; Sequence 105, Application US/08484905

GENERAL INFORMATION:

APPLICANT: Motterz, Estelle

APPLICANT: Ababado, Jean-Pierre

APPLICANT: Kourilsky, Philippe

TITLE OF INVENTION: An Altered Major Histocompatibility Complex (MHC) Determinant and Methods for Using the

TITLE OF INVENTION: Determinant

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 ADDRESSEE: Dunner  
 STREET: 1300 I Street, N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/484, 905  
 FILING DATE: 07-JUNE-1995  
 CLASSIFICATION: 530  
 PRIORITY DATA:  
 PRIORITY NUMBER: US 07/801, 818  
 FILING DATE: 05-DEC-1991  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/792, 473  
 FILING DATE: 15-NOV-1991  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Potter, Jane E. R.  
 REGISTRATION NUMBER: 33, 332  
 REFERENCE/DOCKET NUMBER: 03495.0106-03000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 105:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 274 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-08-484-905-105

Query Match 8.0%; Score 29; DB 2; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-19;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 QTQDTELVERPAGDTFQRKWAAYVPSG 273  
 Db 224 QTQDTELVERPAGDTFQRKWAAYVPSG 252

Search completed: July 13, 2005, 09:24:23  
 Job time : 44 secs

Copyright GenCore version 5.1.6  
 (C) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 09:14:49 ; Search time 163 Seconds  
 (without alignment)

Scoring table: 857.989 Million cell updates/sec

Title: US-09-819-371-4

Pearfect score: 362

Sequence: 1 MAPRSLLLGSALALTDTW.....QAATDSAQSGSVLTANKV 362

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1726220 seqs, 386332138 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.\*

1: /cggn2\_6/ptodata/1/pubbaa/US07\_PUBCOMB.pep.\*  
 2: /cggn2\_6/ptodata/1/pubbaa/PCT NEW PUB.pep.\*  
 3: /cggn2\_6/ptodata/1/pubbaa/US06\_NEW PUB.pep.\*  
 4: /cggn2\_6/ptodata/1/pubbaa/US06\_PUBCOMB.pep.\*  
 5: /cggn2\_6/ptodata/1/pubbaa/US07\_NEW PUB.pep.\*  
 6: /cggn2\_6/ptodata/1/pubbaa/PCTUS\_PUBCOMB.pep.\*  
 7: /cggn2\_6/ptodata/1/pubbaa/US08\_NEW PUB.pep.\*  
 8: /cggn2\_6/ptodata/1/pubbaa/US08\_PUBCOMB.pep.\*  
 9: /cggn2\_6/ptodata/1/pubbaa/US09\_PUBCOMB.pep.\*  
 10: /cggn2\_6/ptodata/1/pubbaa/US09B\_PUBCOMB.pep.\*  
 11: /cggn2\_6/ptodata/1/pubbaa/US09C\_PUBCOMB.pep.\*  
 12: /cggn2\_6/ptodata/1/pubbaa/US09\_NNEW PUB.pep.\*  
 13: /cggn2\_6/ptodata/1/pubbaa/US10A\_PUBCOMB.pep.\*  
 14: /cggn2\_6/ptodata/1/pubbaa/US10B\_PUBCOMB.pep.\*  
 15: /cggn2\_6/ptodata/1/pubbaa/US10C\_PUBCOMB.pep.\*  
 16: /cggn2\_6/ptodata/1/pubbaa/US10E\_PUBCOMB.pep.\*  
 17: /cggn2\_6/ptodata/1/pubbaa/US10F\_PUBCOMB.pep.\*  
 18: /cggn2\_6/ptodata/1/pubbaa/US10\_NNEW PUB.pep.\*  
 19: /cggn2\_6/ptodata/1/pubbaa/US11A\_PUBCOMB.pep.\*  
 20: /cggn2\_6/ptodata/1/pubbaa/US11\_NNEW PUB.pep.\*  
 21: /cggn2\_6/ptodata/1/pubbaa/US60\_NEW PUB.pep.\*  
 22: /cggn2\_6/ptodata/1/pubbaa/US60\_PUBCOMB.pep.\*

RESULT 1

US-09-819-371-4

; Sequence 4, Application US/09819371  
 ; Publication No. US200400533441  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Egrwa, Kohji  
 ; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can  
 ; FILE REFERENCE: 30815  
 ; CURRENT APPLICATION NUMBER: US/09/819,371  
 ; CURRENT FILING DATE: 2002-03-15  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SEQ ID NO 4  
 ; LENGTH: 362  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-819-371-4

## SUMMARIES

## ALIGNMENTS

Query Match Score 362; DB 11; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 362; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 MAPRSLLLGSALALTDTWAGSHSLRYFSTAVSRPGRGEPRYAVYVDDTOFLRFPSD 60  
 Db 1 MAPRSLLLGSALALTDTWAGSHSLRYFSTAVSRPGRGEPRYAVYVDDTOFLRFPSD 60

Sequence 4, Appli  
 Sequence 82, Appli  
 Sequence 187, Ap  
 Sequence 1431, Ap  
 Sequence 6, Appli  
 Sequence 4063, Ap  
 Sequence 8, Appli  
 Sequence 363, Appli  
 Sequence 1135, Ap  
 Sequence 387, Ap  
 Sequence 1143, Ap  
 Sequence 8, Appli  
 Sequence 384, Ap  
 Sequence 1142, Ap  
 Sequence 3648, Ap  
 Sequence 7, Appli  
 Sequence 10, Appli  
 Sequence 380, Ap  
 Sequence 388, Ap  
 Sequence 1134, Ap  
 Sequence 1138, Ap  
 Sequence 110, Ap  
 Sequence 343, Ap  
 Sequence 379, Ap  
 Sequence 1139, Ap  
 Sequence 78, Ap  
 Sequence 160, Ap  
 Sequence 8, Appli  
 Sequence 28883, A  
 Sequence 3561, A  
 Sequence 799, Ap  
 Sequence 2139, Ap  
 Sequence 799, Ap  
 Sequence 2139, Ap

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	362	100.0	362	11 US-09-819-371-4	Sequence 4, Appli
2	261	72.1	362	15 US-10-25-021-82	Sequence 82, Appli
3	244	67.4	442	16 US-10-408-762A-1897	Sequence 187, Ap
4	196	54.1	271	9 US-09-925-301-1431	Sequence 1431, Ap
5	175	48.3	274	11 US-09-819-371-5	Sequence 6, Appli
6	95	26.2	215	11 US-09-819-371-6	Sequence 4063, Ap
7	70	19.3	186	15 US-10-264-049-4063	Sequence 8, Appli
8	68	18.8	96	14 US-10-309-386-30718	Sequence 30718, A
9	44	12.2	77	14 US-10-023-386-344273	Sequence 344273, A
10	44	12.2	91	14 US-10-029-386-31089	Sequence 31089, A
11	44	12.2	104	9 US-09-925-302-835	Sequence 835, Ap

*Authentic*

Qy 181 LEGCCLLRLRYLENGLETQRADPPKXVAHPISDHEATRCWALGFYPAEITLTWQR 240  
 Db 181 LEGCCLLRLRYLENGLETQRADPPKXVAHPISDHEATRCWALGFYPAEITLTWQR 240  
 Qy 241 DGBEQQTQTELVETRPAGDTGFTKWAATVVPSEGEORTCHYQHEGLPQPLTLRWEQS PQ 300  
 Db 241 DGBEQQTQTELVETRPAGDTGFTKWAATVVPSEGEORTCHYQHEGLPQPLTLRWEQS PQ 300  
 Qy 301 PTIPVGIVAGLVVLAGVUTGAVVAAWMRKCSSDRNGSYSSQAATDSAQGSVSLTAN 360  
 Db 301 PTIPVGIVAGLVVLAGVUTGAVVAAWMRKCSSDRNGSYSSQAATDSAQGSVSLTAN 360  
 Qy 361 KV 362  
 Db 361 KV 362

RESULT 2  
 US-10-257-021-82  
 Sequence 82, Application US/10257021  
 Publication No. US20030211498A1  
 GENERAL INFORMATION:  
 APPLICANT: Morin, Patrice J.  
 PRIORITY: Sherman-Bauer, Cheryl A.  
 APPLICANT: Pfizer, Ellen S.  
 APPLICANT: Hough, Colleen D.  
 TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER  
 FILE REFERENCE: 1414.0369U2  
 CURRENT APPLICATION NUMBER: US/10/257,021  
 PRIOR APPLICATION NUMBER: PCT/US01/10947  
 PRIOR FILING DATE: 2002-10-03  
 PRIOR APPLICATION NUMBER: 60/194,336  
 PRIOR FILING DATE: 2000-04-03  
 NUMBER OF SEQ ID NOS: 147  
 SOFTWARE: Fast-SEQ for Windows Version 4.0  
 SEQ ID NO 82  
 LENGTH: 362  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-257-021-82

Query Match 72.1%; Score 261; DB 15; Length 362;  
 Best Local Similarity 99.7%; Pred. No. 1e-233; Indels 0; Gaps 0;  
 Matches 361; Conservative 0; Mismatches 1;

Qy 1 MARSLLLISGALALTWTAGSHSLRVFSTAVSRPGEPYIAVEYVDDTQFLRFSD 60  
 Db 1 MARSLLLISGALALTWTAGSHSLRVFSTAVSRPGEPYIAVEYVDDTQFLRFSD 60  
 Qy 61 AAIPRMEPREPWPVQEQQWENTTGYZAKANACTDRLNLLRNVFSTAVSRPGE PYIAVEYVDDTQFLRFSD 60  
 Db 61 AAIPRMEPREPWPVQEQQWENTTGYZAKANACTDRLNLLRNVFSTAVSRPGE PYIAVEYVDDTQFLRFSD 60  
 Qy 121 GCDMGPDRLLRQHHDYGDGYISNEDLSWTAADTVQITOREYEAEFRTY 180  
 Db 121 GCDMGPDRLLRQHHDYGDGYISNEDLSWTAADTVQITOREYEAEFRTY 180  
 Qy 181 LEGCCLLRLRYLENGLETQRADPPKXVAHPISDHEATRCWALGFYPAEITLTWQR 240  
 Db 181 LEGCCLLRLRYLENGLETQRADPPKXVAHPISDHEATRCWALGFYPAEITLTWQR 240  
 Qy 241 DGBEQQTQTELVETRPAGDTGFTKWAATVVPSEGEORTCHYQHEGLPQPLTLRWEQS PQ 300  
 Db 241 DGBEQQTQTELVETRPAGDTGFTKWAATVVPSEGEORTCHYQHEGLPQPLTLRWEQS PQ 300  
 Qy 301 PTIPVGIVAGLVVLAGVUTGAVVAAWMRKCSSDRNGSYSSQAATDSAQGSVSLTAN 360  
 Db 301 PTIPVGIVAGLVVLAGVUTGAVVAAWMRKCSSDRNGSYSSQAATDSAQGSVSLTAN 360  
 Qy 361 KV 362

RESULT 3  
 US-10-408-765A-1887  
 Sequence 1887, Application US/10408765A  
 Publication No. US20040101874A1  
 GENERAL INFORMATION:  
 APPLICANT: Ghosh, Soumitra S.  
 APPLICANT: Fahy, Boin D.  
 APPLICANT: Zhang, Bing  
 APPLICANT: Gibson, Bradford W.  
 APPLICANT: Taylor, Steven W.  
 APPLICANT: Glenn, Gary M.  
 APPLICANT: Warnock, Dale E.  
 TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
 FILE REFERENCE: 660088,465  
 CURRENT APPLICATION NUMBER: US/10/408,765A  
 CURRENT FILING DATE: 2003-04-04  
 NUMBER OF SEQ ID NOS: 3077  
 SOFTWARE: Fast-SEQ for Windows Version 4.0  
 SEQ ID NO 1887

Query Match 67.4%; Score 244; DB 16; Length 442;  
 Best Local Similarity 99.7%; Pred. No. 7.6e-218; Indels 0; Gaps 0;  
 Matches 344; Conservative 0; Mismatches 1;

Qy 1 MAPRSLLLISGALALTWTAGSHSLRVFSTAVSRPGEPYIAVEYVDDTQFLRFSD 60  
 Db 1 MAPRSLLLISGALALTWTAGSHSLRVFSTAVSRPGEPYIAVEYVDDTQFLRFSD 60  
 Qy 61 AAIPRMEPREPWPVQEQQWENTTGYZAKANACTDRLNLLRNVFSTAVSRPGE PYIAVEYVDDTQFLRFSD 60  
 Db 61 AAIPRMEPREPWPVQEQQWENTTGYZAKANACTDRLNLLRNVFSTAVSRPGE PYIAVEYVDDTQFLRFSD 60  
 Qy 121 GCDMGPDRLLRQHHDYGDGYISNEDLSWTAADTVQITOREYEAEFRTY 180  
 Db 121 GCDMGPDRLLRQHHDYGDGYISNEDLSWTAADTVQITOREYEAEFRTY 180  
 Qy 181 LEGCCLLRLRYLENGLETQRADPPKXVAHPISDHEATRCWALGFYPAEITLTWQR 240  
 Db 181 LEGCCLLRLRYLENGLETQRADPPKXVAHPISDHEATRCWALGFYPAEITLTWQR 240  
 Qy 241 DGEETQDTVELTVERPAGDTGTFQKWAAYVPSGEORYTCVQHEGLPQPLTLRWEQS PQ 300  
 Db 241 DGEETQDTVELTVERPAGDTGTFQKWAAYVPSGEORYTCVQHEGLPQPLTLRWEQS PQ 300  
 Qy 301 PTIPVGIVAGLVVLAGVUTGAVVAAWMRKCSSDRNGSYSSQAATDSAQGSVSLTAN 345  
 Db 301 PTIPVGIVAGLVVLAGVUTGAVVAAWMRKCSSDRNGSYSSQAATDSAQGSVSLTAN 345

RESULT 4  
 US-09-925-101-1431  
 Sequence 1431, Application US/09925301  
 Patent No. US20052308A1  
 GENERAL INFORMATION:  
 APPLICANT: Rogin et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 FILE REFERENCE: PA106  
 CURRENT APPLICATION NUMBER: US/09/925,301  
 CURRENT FILING DATE: 2001-08-10  
 PRIOR APPLICATION NUMBER: PCT/US00/05882  
 PRIOR FILING DATE: 2000-03-08  
 PRIOR APPLICATION NUMBER: 60/124,270  
 PRIOR FILING DATE: 1999-03-12  
 NUMBER OF SEQ ID NOS: 1694  
 SOFTWARE: PatentIn Ver. 2.0

*PatentIn 02/02/02*

SEQ ID NO: 1431  
*i LENGTH: 271*  
*i TYPE: PRT*  
*i ORGANISM: Homo sapiens*  
US-09-925-301-1431

Query Match 54.1%; Score 196; DB 9; Length 271;  
Best Local Similarity 100.0%; Pred. No. 2e-173;  
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRSLLLISGALALTDTWAGSHSLRYFSTAVSRPGRGEPRYIAVEYDDTQFLRFSD 60  
Db 7 MAPRSLLLISGALALTDTWAGSHSLRYFSTAVSRPGRGEPRYIAVEYDDTQFLRFSD 66

61 AAIPRMPREPWPWEGPQYWETWTGYAKANAQTDRAVLNLLRRYNQSEAGSHTLQZN 120  
Db 67 AAIPRMPREPWPWEGPQYWETWTGYAKANAQTDRAVLNLLRRYNQSEAGSHTLQZN 126

QY 121 GCDMGDPGRLLRGYHQHDGKDYLISLNEDLRSWTAADTVQAQTORFYEAEEFRITY 180  
Db 127 GCDMGDPGRLLRGYHQHDGKDYLISLNEDLRSWTAADTVQAQTORFYEAEEFRITY 186

QY 181 LEGECLLERLRYLENG 196  
Db 187 LEGECLLERLRYLENG 202

RESULT 7  
US-10-264-049-4063  
*i Sequence 4063, Application US/10264049*  
*i Publication No. US20040005579A1*

GENERAL INFORMATION:  
*i APPLICANT: Bire et al.*  
*i TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies*  
*i FILE REFERENCE: PAI3JPL*  
*i CURRENT APPLICATION NUMBER: US/10/264,049*  
*i CURRENT FILING DATE: 2002-10-04*  
*i PRIOR APPLICATION NUMBER: PCT/US01/18559*  
*i PRIORITY DATE: 2001-06-07*  
*i PRIORITY APPLICATION NUMBER: US 60/209,467*  
*i PRIORITY FILING DATE: 2000-06-07*  
*i NUMBER OF SEQ ID NOS: 4360*  
*i SOFTWARE: PatentIn Ver. 3.1*  
*i SEQ ID NO 4063*  
*i LENGTH: 186*  
*i TYPE: PRT*  
*i ORGANISM: Homo sapiens*  
*i FEATURE: NAME/KEY: MISC\_FEATURE*  
*i LOCATION: (76)\_FEATURE*  
*i OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids*  
*i FEATURE: NAME/KEY: MISC\_FEATURE*  
*i LOCATION: (77)\_FEATURE*  
*i OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids*  
*i FEATURE: NAME/KEY: MISC\_FEATURE*  
*i LOCATION: (86)\_FEATURE*  
*i OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids*  
*i FEATURE: NAME/KEY: MISC\_FEATURE*  
*i LOCATION: (107)\_FEATURE*  
*i OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids*  
*i FEATURE: NAME/KEY: MISC\_FEATURE*  
*i LOCATION: (124)\_FEATURE*  
*i OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids*  
*i FEATURE: NAME/KEY: MISC\_FEATURE*  
*i LOCATION: (135)\_FEATURE*  
*i OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids*  
*i FEATURE: NAME/KEY: MISC\_FEATURE*  
*i LOCATION: (148)\_FEATURE*  
*i OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids*

SEQ ID NO: 5  
*i Sequence 5, Application US/0919371*  
*i Publication No. US20040053344A1*

GENERAL INFORMATION:  
*i APPLICANT: Egawa, Kohji*  
*i TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Cancer*  
*i FILE REFERENCE: 30815*  
*i CURRENT APPLICATION NUMBER: US/09/819,371*  
*i CURRENT FILING DATE: 2002-03-15*  
*i NUMBER OF SEQ ID NOS: 6*  
*i SOFTWARE: PatentIn version 3.0*  
*i SEQ ID NO 5*  
*i LENGTH: 274*  
*i TYPE: PRT*  
*i ORGANISM: Homo sapiens*  
US-09-819-371-5

Query Match 48.3%; Score 175; DB 11; Length 274;  
Best Local Similarity 100.0%; Pred. No. 6.6e-154;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GHSHSLRYFSTAVSRPGRGEPRYIAVEYDDTQFLRFSDAAIPMNEPRPWVQEGPQYW 81  
Db 1 GHSHSLRYFSTAVSRPGRGEPRYIAVEYDDTQFLRFSDAAIPMNEPRPWVQEGPQYW 60

82 EWTGTYAKANAQTDRAVLNLLRRYNQSEAGSHTLQZNEDLRSWTAADTVQAQTORFYEAEEFRITY 141  
Db 61 EWTGTYAKANAQTDRAVLNLLRRYNQSEAGSHTLQZNEDLRSWTAADTVQAQTORFYEAEEFRITY 140

QY 142 KDYISLNEDLRSWTAADTVQAQTORFYEAEEFRITYLEGCECLLRLRYLENG 196  
Db 121 KDYISLNEDLRSWTAADTVQAQTORFYEAEEFRITYLEGCECLLRLRYLENG 175

RESULT 6  
US-09-819-371-6  
*i Sequence 6, Application US/0919371*  
*i Publication No. US20040053344A1*

GENERAL INFORMATION:  
*i APPLICANT: Egawa, Kohji*  
*i TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Cancer*  
*i FILE REFERENCE: 30815*  
*i CURRENT APPLICATION NUMBER: US/09/819,371*

OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

FEATURE: MISC FEATURE  
NAME/KEY: MISC FEATURE  
LOCATION: (163)  
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

FEATURE: MISC FEATURE  
NAME/KEY: MISC FEATURE  
LOCATION: (174)  
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

FEATURE: MISC FEATURE  
NAME/KEY: MISC FEATURE  
LOCATION: (175)  
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

FEATURE: MISC FEATURE  
NAME/KEY: MISC FEATURE  
LOCATION: (180)  
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

US-10-264-049-4053

Query Match 19.3%; Score 70; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.7e-56;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 YAKANACTDVALRNLLRYNQSBEAGSHTLQGMNGCDMGPDRGLLRCYHQAYDGKDYIS 146  
Db 1 YAKANACTDVALRNLLRYNQSBEAGSHTLQGMNGCDMGPDRGLLRCYHQAYDGKDYIS 60

Qy 147 LNEDLRSITA 156  
Db 61 LNEDLRSITA 70

---

RESULT 8  
US-10-029-386-30718  
Sequence 30718, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C FILE REFERENCE: AEOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SEQ ID NO: 30718  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR6.1  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12  
OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUO 2.00e-52  
US-10-029-386-30718

Query Match 18.8%; Score 68; DB 14; Length 96;  
Best Local Similarity 100.0%; Pred. No. 7e-55;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 204 DPPKAHYHHPISDHEATLRCWALGFYPAEITLTWORDGEROTDTELVERTPAGDTFQ 263  
Db 2 DPPKAHYHHPISDHEATLRCWALGFYPAEITLTWORDGEROTDTELVERTPAGDTFQ 61

---

RESULT 9  
US-10-029-386-34273  
Sequence 34273, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Rank, David R.  
APPLICANT: Hanel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C FILE REFERENCE: AEOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SEQ ID NO: 34273  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR6.1  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1  
OTHER INFORMATION: SWISSPROT HIT: P30509, EVALUO 1.00e-52  
US-10-029-386-31089

Query Match 12.2%; Score 44; DB 14; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1.3e-32;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 QTQDTTELVERTPAGDTFQKMAAVVPSGEQRTCHVQHEGLP 288  
Db 41 QTQDTTELVERTPAGDTFQKMAAVVPSGEQRTCHVQHEGLP 84

RESULT 11  
US-09-925-302-835  
Sequence 835, Application US/09925302  
Patent No. US20020041941A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA104  
CURRENT APPLICATION NUMBER: US/09/925,302  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05918  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 896  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 835  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (95)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-302-835

Query Match 12.2%; Score 44; DB 9; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.5e-32;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 QTQDTTELVTRPAGDTFQRKWAAVVPSGEQRTCHYQHEGLP 288  
Db 32 QTQDTTELVTRPAGDTFQRKWAAVVPSGEQRTCHYQHEGLP 75

RESULT 12  
US-09-925-302-835  
Sequence 835, Application US/09925302  
Publication No. US20030064072A9  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA104  
CURRENT APPLICATION NUMBER: US/09/925,302  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05918  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 896  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 835  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (95)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-302-835

Query Match 12.2%; Score 44; DB 10; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.5e-32;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 QTQDTTELVTRPAGDTFQRKWAAVVPSGEQRTCHYQHEGLP 288  
Db 32 QTQDTTELVTRPAGDTFQRKWAAVVPSGEQRTCHYQHEGLP 75

RESULT 13  
US-10-741-600-941  
Sequence 941, Application US/10741600  
Publication No. US200500216169A1  
GENERAL INFORMATION:  
APPLICANT: Cargill, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001499  
CURRENT APPLICATION NUMBER: US/10/741,600  
CURRENT FILING DATE: 2003-12-22  
NUMBER OF SEQ ID NOS: 73997  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 941  
LENGTH: 365  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-741-600-941

Query Match 12.2%; Score 44; DB 17; Length 365;  
Best Local Similarity 100.0%; Pred. No. 4.6e-32;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 QTQDTTELVTRPAGDTFQRKWAAVVPSGEQRTCHYQHEGLP 288  
Db 248 QTQDTTELVTRPAGDTFQRKWAAVVPSGEQRTCHYQHEGLP 291

RESULT 14  
US-10-430-984-16  
Sequence 16, Application US/10430984  
Publication No. US20040225112A1  
GENERAL INFORMATION:  
APPLICANT: The Board of Trustees of the University of Arkansas  
FILE REFERENCE: 8793-53098  
TITLE OF INVENTION: Proteins Encoding Single Chain Human Leukocyte Antigen E (HLA-E)  
TITLE OF INVENTION: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity  
CURRENT APPLICATION NUMBER: US/10/430,984  
CURRENT FILING DATE: 2003-05-09  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO: 16  
LENGTH: 476  
TYPE: PRT  
ORGANISM: human leukocyte antigen E-Single chain dimer  
US-10-430-984-16

Query Match 11.9%; Score 43; DB 16; Length 476;  
Best Local Similarity 100.0%; Pred. No. 5e-31;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 TQDTTELVTRPAGDTFQRKWAAVVPSGEQRTCHYQHEGLP 288  
Db 364 TQDTTELVTRPAGDTFQRKWAAVVPSGEQRTCHYQHEGLP 406

RESULT 15  
US-10-430-984-15  
Sequence 15, Application US/10430984  
Publication No. US20040225112A1  
GENERAL INFORMATION:  
APPLICANT: The Board of Trustees of the University of Arkansas  
FILE REFERENCE: 8793-53098  
CURRENT APPLICATION NUMBER: US/10/430,984  
CURRENT FILING DATE: 2003-05-09  
NUMBER OF SEQ ID NOS: 16  
SEQ ID NO: 15  
LENGTH: 500  
TYPE: PRT  
ORGANISM: human leukocyte antigen E-Single chain Trimer  
US-10-430-984-15

us-10-430-984-15

Query Match      11.9%;    Score 43;    DB 16;    Length 500;  
Best Local Similarity      100.0%;    Pred. No. 5.2e-31;  
Matches      43;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;  
Qy      246 TQDTTELVTRPAGDGTQKWAAVVVPSGEEQRTCHVQHEGLP 288  
          ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db      388 TQDTTELVTRPAGDGTQKWAAVVVPSGEEQRTCHVQHEGLP 430

Search completed: July 13, 2005, 09:28:24  
Job time : 164 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:59:16 ; Search time 164 Seconds  
(without alignments)  
853.703 Million cell updates/sec

Title: US-09-819-371-4  
Perfect score: 362  
Sequence: 1 MAPRSILLISGALALTDTW.....QAAVTDQAQSGCVLTANKV 362

Scoring table: OLFIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseqp\_16Dec04:  
1: Geneseqp1980s:  
2: Geneseqp1990s:  
3: Geneseqp000s:  
4: Geneseqp2001s:  
5: Geneseqp2002s:  
6: Geneseqp2003as:  
7: Geneseqp2003bs:  
8: Geneseqp2004s:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	AAG64617	362	4	AAG64617	AAG64617 Human can	
2	ABB50296	362	4	ABB50296	Abb50296 HLA-Cw ov	
3	ADP12500	362	7	ADP12500	Adp12500 Protein e	
4	ADJ75372	362	8	ADJ75372	Adj75372 Marker ge	
5	ABM80784	362	8	ABM80784	Abm80784 Tumour-as	
6	ADP23768	362	8	ADP23768	Adp23768 PRO polyp	
7	ADS10818	362	8	ADS10818	AdS10818 Human the	
8	ADP14305	362	8	ADP14305	Adp14305 PRO polyp	
9	ADP12206	362	7	ADP12206	Adp12206 Novel hum	
10	AAB43986	349	8	AAB43986	Aab43986 Human can	
11	ABG64618	677	4	ABG64618	Abg64618 Novel hum	
12	AAG64616	48.3	274	AAG64616	Aag64616 Human can	
13	ADP55588	48.3	274	ADP55588	Adp55588 Fragment	
14	AAG64619	42.3	215	AAG64619	Aag64619 Human can	
15	ADP55589	42.3	215	ADP55589	Adp55589 Fragment	
16	ADQ65964	40.9	349	ADQ65964	Adq65964 Novel hum	
17	AG00209	33.1	120	AG00209	Ag00209 Human sec	
18	ADP12106	20.4	120	ADP12106	Adp12106 Novel hum	
19	ABP42931	19.3	186	ABP42931	Abp42931 Human ova	
20	ABO657084	18.8	96	ABO657084	Abo657084 Human gen	
21	ABO57455	12.2	77	ABO57455	Abo57455 Human gen	
22	ABO57455	12.2	91	ABO57455	Abo57455 Human gen	
23	AAP80911	12.2	104	AAP80911	Aap80911 Lung canc	
24	AAP80911	12.2	274	AAP80911	Aap80911 Consensus	
25	ADP12521	12.2	365	ADP12521	Adp12521 Protein e	

## ALIGNMENTS

RESULT 1:  
AA64617

ID AA64617 standard; protein: 362 AA.  
XX  
AC  
XX DT 12-SEP-2001 (first entry)  
XX Human cancer cell specific HLA-F antigen SEQ ID 4.  
DE XX  
KW XX  
OS Homo sapiens  
XX PN JP001095584-A.  
XX PD 10-APR-2001.  
XX PF 30-SEP-1999; 99JP-00279566.  
XX PR 30-SEP-1999; 99JP-00279566.  
XX PR 30-SEP-1999; 99JP-00279566.

\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	AAG64617	362	4	AAG64617	AAG64617 Human can	
2	ABB50296	362	4	ABB50296	Abb50296 HLA-Cw ov	
3	ADP12500	362	7	ADP12500	Adp12500 Protein e	
4	ADJ75372	362	8	ADJ75372	Adj75372 Marker ge	
5	ABM80784	362	8	ABM80784	Abm80784 Tumour-as	
6	ADP23768	362	8	ADP23768	Adp23768 PRO polyp	
7	ADS10818	362	8	ADS10818	AdS10818 Human the	
8	ADP14305	362	8	ADP14305	Adp14305 PRO polyp	
9	ADP12206	362	7	ADP12206	Adp12206 Novel hum	
10	AAB43986	349	8	AAB43986	Aab43986 Human can	
11	ABG64618	677	4	ABG64618	Abg64618 Novel hum	
12	AAG64616	48.3	274	AAG64616	Aag64616 Human can	
13	ADP55588	48.3	274	ADP55588	Adp55588 Fragment	
14	AAG64619	42.3	215	AAG64619	Aag64619 Human can	
15	ADP55589	42.3	215	ADP55589	Adp55589 Fragment	
16	ADQ65964	40.9	349	ADQ65964	Adq65964 Novel hum	
17	AG00209	33.1	120	AG00209	Ag00209 Human sec	
18	ADP12106	20.4	120	ADP12106	Adp12106 Novel hum	
19	ABP42931	19.3	186	ABP42931	Abp42931 Human ova	
20	ABO657084	18.8	96	ABO657084	Abo657084 Human gen	
21	ABO57455	12.2	77	ABO57455	Abo57455 Human gen	
22	ABO57455	12.2	91	ABO57455	Abo57455 Human gen	
23	AAP80911	12.2	104	AAP80911	Aap80911 Lung canc	
24	AAP80911	12.2	274	AAP80911	Aap80911 Consensus	
25	ADP12521	12.2	365	ADP12521	Adp12521 Protein e	

Query Match 72.1%; Score 261; DB 4; Length 362;  
Best Local Similarity 99.7%; Predict. No. 1.e-229;  
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAPRLSLILNLISGALALTDIWGSILRYSTAVSRPGCEPRYIAVEYVDDTQLRLFDSD 60

Db 1 MAPSLLULSGALATIWGSHSLRFSTAVSRPGRGEPRVIAVEYVDDDFQFLRPSD 60  
 Qy 61 AAIPRMEEPREPWFVQEQQYQWENTTG/YAKANAOQTDRV/LRNLLRYNQSEASHTLQGMN 120  
 Qy 61 AAIPRMEEPREPWFVQEQQYQWENTTG/YAKANAOQTDRV/LRNLLRYNQSEASHTLQGMN 120  
 Db 121 GCDMGPDGRLLRGYHQHAYDGYD/YISNEDLSWTAAQITQTYEAEYVAEPRTY 180  
 Qy 181 LEGCCLERLRLRYLNGLETLQRADPPKAKVHHPISDEAHLRCWALGFYPAEITLW QR 240  
 Db 181 LEGCCLERLRLRYLNGKETLQRADPPKAKVHHPISDEAHLRCWALGFYPAEITLW QR 240  
 Db 241 DGEBOQTQDTLEVTRPAGDTGPQKWAAVVPSGEQRTYCHYQHEGLPQPLILRWBOSPQ 300  
 Qy 241 DGEBOQTQDTLEVTRPAGDTGPQKWAAVVPSGEQRTYCHYQHEGLPQPLILRWEQPQ 300  
 Qy 301 PTPIVGVAGLVVLGAVVTTGAVVAAVMWRKGSSDRNGSYSSQAATVDSAQSMSGVSLTN 360  
 Db 301 PTPIVGVAGLVVLGAVVTTGAVVAAVMWRKGSSDRNGSYSSQAATVDSAQSMSGVSLTN 360  
 Qy 361 KV 362  
 Db 361 KV 362

**RESULT 2**  
 ID ABB50296 standard; protein; 362 AA.  
 XX ABB50296;  
 XX DT 08-FEB-2002 (first entry)  
 DE HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.

Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; mucinous cystadenocarcinoma; borderline mucinous tumour; endometrioid carcinoma; undifferentiated carcinoma; clear cell adenocarcinoma; cystadenocarcinoma; adenofibroma; Brenner tumor; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic; gene therapy; vaccine.  
 Homo sapiens.  
 XX WO200175177-A2.  
 XX PD 11-OCT-2001.  
 XX PP 03-APR-2001; 2001WO-US010947.  
 XX PR 03-APR-2000; 2000US-0194336P.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;  
 XX DR WPI: 2001-626450/72.  
 XX N-PSDB; ABA83122.

Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker gene.

Claim 23; Page 126-127; 14Opp; English.

The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180, ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179, ABA83181 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer in prognostic tests for assessing the relative severity of ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as an ovarian tumour (i.e., an epithelial ovarian tumour selected from serious cystadenoma, borderline serous tumour, serous cystadenocarcinoma, mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma, adenofibroma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membrane-localised or secreted. In addition to their use as diagnostic and prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABB50257-ABB5099 represent proteins encoded by ovarian tumour genes of the invention.

Sequence 362 AA:

Query	Match	Score	Length
	Best Local Similarity	261;	362;
	Matches	99.7%	Pred. No. 1.4e-229;
	Indels	0;	Gaps 0;
Qy	1 MAPRSILLISCALTDTWGSHSLRYFSTAVSRPGRGEPRVIAVEYVDDDFQFLRPSD	60	
Db	1 MAPRSILLISCALTDTWGSHSLRYFSTAVSRPGRGEPRVIAVEYVDDDFQFLRPSD	60	
Qy	61 AAIPRMEEPREPWFVQEQQYQWENTTG/YAKANAOQTDRV/LRNLLRYNQSEASHTLQGMN	120	
Db	61 AAIPRMEEPREPWFVQEQQYQWENTTG/YAKANAOQTDRV/LRNLLRYNQSEASHTLQGMN	120	
Qy	121 GCDMGPDGRLLRGYHQHAYDGYD/YISNEDLSWTAAQITQTYEAEYVAEPRTY	180	
Db	121 GCDMGPDGRLLRGYHQHAYDGYD/YISNEDLSWTAAQITQTYEAEYVAEPRTY	180	
Qy	181 LEGCCLERLRLRYLNGLETLQRADPPKAKVHHPISDEAHLRCWALGFYPAEITLW	240	
Db	181 LEGCCLERLRLRYLNGKETLQRADPPKAKVHHPISDEAHLRCWALGFYPAEITLW	240	
Qy	241 DGEBOQTQDTLEVTRPAGDTGPQKWAAVVPSGEQRTYCHYQHEGLPQPLILRWBOSPQ	300	
Db	241 DGEBOQTQDTLEVTRPAGDTGPQKWAAVVPSGEQRTYCHYQHEGLPQPLILRWBOSPQ	300	
Qy	301 PTIPIVGVAGLVVLGAVVTTGAVVAAVMWRKGSSDRNGSYSSQAATVDSAQSMSGVSLTN	360	
Db	301 PTIPIVGVAGLVVLGAVVTTGAVVAAVMWRKGSSDRNGSYSSQAATVDSAQSMSGVSLTN	360	

XX RESULT 3

ID	ADFS5587
XX	ADFS5587 standard; protein; 362 AA.
AC	ADFS5587;
XX	AC ADF5587;
DT	12-FEB-2004 (first entry)
XX	XX
PS	Human cancer-cell specific HLA-F antigen.
XX	XX

Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX  
 OS Homo sapiens.  
 XX  
 JP2003012544-A.  
 XX  
 15-JAN-2003.  
 PD  
 XX  
 PF 27-MAR-2002; 2002JP-00088991.  
 XX  
 PR 27-MAR-2001; 2001JP-00090121.  
 XX  
 PA (EGAWA/ ) EGAWA K.  
 PA (MEDIN/ ) MEDINT' KK.  
 PA (KIMU/ ) KIMURA Y.  
 DR WPI: 2003-486263 /46.  
 DR N-PSDB; ADF55584.  
 XX  
 PT Agent for preventing and treating cancer, comprising human leukocyte  
 PR antigen-F DNA, or a plasmid or viral vector comprising the DNA.  
 XX  
 PS SEQ ID NO 4; 19PP; Japanese.  
 XX  
 Claim 5; SEQ ID NO 4; 19PP; Japanese.

The present invention relates to an agent for preventing or treating cancer. The agent comprises a portion or a complete sequence of a human leukocyte antigen (HLA)-F gene. Also disclosed is a cell capable of presenting a cancer-cell specific antigen transformed with HLA-F DNA, or a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte (CTL) inducer which induces CTL which is non-specific to an organ, is unrestricted to the major histocompatibility complex (MHC) and specific to a cancer cell, and an anti-HLA-F antibody. The agent of the invention is useful for treating or preventing cancer. A cell capable of presenting a cancer-cell specific antigen is useful for measuring HLA-F antigen and for diagnosing cancer. The present sequence represents human cancer-cell specific HLA-F antigen.

XX  
 SQ Sequence 362 AA:  
 Query Match Score 261; DB 7; Length 362;  
 Best Local Similarity 99.7%; Pred. No. 1.4e-229;  
 Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1 MAPSLLLISGALDTWAGSHSLRVTAVSRPGPGEPRVATEYDDTDLRFSD 60
Db	1 MAPSLLLISGALDTWAGSHSLRVTAVSRPGPGEPRVATEYDDTDLRFSD 60
QY	61 AAIPRMPEPREPWVEQGPQYWENTWGYAKANAQTDRAVLNLRLRYNQSEAGSHTLQGMN 120
Db	61 AAIPRMPEPREPWVEQGPQYWENTWGYAKANAQTDRAVLNLRLRYNQSEAGSHTLQGMN 120
QY	121 GCDMGPDRILLRGHQAHDGKDVSILNEEDLSRSTAATDVAQTQRFEEAEFFTY 180
Db	121 GCDMGPDRILLRGHQAHDGKDVSILNEEDLSRSTAATDVAQTQRFEEAEFFTY 180
QY	181 LEGELELLIRRYLENGLETIQLRADPKPAIKAHHPSIDHEATLRWALGYPAPAETTLWQR 240
Db	181 LEGELELLIRRYLENGLETIQLRADPKPAIKAHHPSIDHEATLRWALGYPAPAETTLWQR 240
QY	241 DGEETOTDTEVELTRPAGDTFQKWAAYVPSGEQRVTCYQHEGLQPLLIRWEQSPQ 300
Db	241 DGEETOTDTEVELTRPAGDTFQKWAAYVPSGEQRVTCYQHEGLQPLLIRWEQSPQ 300
QY	301 PTIPVGIVAGLVVGLGAVVAVMRKSSDRNGSYSQAVTVAQGSGVSLTAN 360
Db	301 PTIPVGIVAGLVVGLGAVVAVMRKSSDRNGSYSQAVTVAQGSGVSLTAN 360
QY	361 KV 362
Db	361 KV 362

Sequence 362 AA:  
 Query Match Score 261; DB 8; Length 362;  
 Best Local Similarity 99.7%; Pred. No. 1.e-229;

Matches	361;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	1 MAPRSLLLSCALALTDWAGSHSLRYFSTAVSRPGERGPRYIAVEYVDDTQFLRFDSD	60							
Db	1 MAPRSLLLSCALALTDWAGSHSLRYFSTAVSRPGERGPRYIAVEYVDDTQFLRFDSD	60							
Qy	61 AAI PRM PPREPWE QES PQT WTTG YAKA NQ TD RVAL NLL RRY NQ SE ASHT LQ GMN	120							
Db	61 AAI PRM PPREPWE QES PQT WTTG YAKA NQ TD RVAL NLL RRY NQ SE ASHT LQ GMN	120							
Qy	121 GCDMGPDGRLLRGYH OHAY DGDY I SNE DLSW TA DTV QI T QRT EYAE YYAE FRTY	180							
Db	121 GCDMGPDGRLLRGYH OHAY DGDY I SNE DLSW TA DTV QI T QRT EYAE YYAE FRTY	180							
Qy	181 LE GE CLE LL RY L E NG KET L QAD PPKAH VAH H PIS DHE AT LR CW AL GFY PA ET TL TW QR	240							
Db	181 LE GE CLE LL RY L E NG KET L QAD PPKAH VAH H PIS DHE AT LR CW AL GFY PA ET TL TW QR	240							
Qy	241 DGE EQ TD TE VTR PAGD GT FQ KWA VVV VPS GE E O R Y T C H V Q H E G L P Q P L L R W E S P Q	300							
Db	241 DGE EQ TD TE VTR PAGD GT FQ KWA VVV VPS GE E O R Y T C H V Q H E G L P Q P L L R W E S P Q	300							
Qy	301 PTIPIVGIVAGLVLGA VV TGCA VVA VWW R KSS DR NRG S Y S Q AA V T D S A Q G S V S T A N	360							
Db	301 PTIPIVGIVAGLVLGA VV TGCA VVA VWW R KSS DR NRG S Y S Q AA V T D S A Q G S V S T A N	360							
Qy	361 KV 362								
Db	361 KV 362								
RESULT 5									
ID	ADP12500 standard; protein; 362 AA.								
XX									
AC	ADP12500;								
XX									
DT	12-AUG-2004 (first entry)								
DE	Protein encoded by mRNA of the invention #110.								
XX	transplant rejection; immune system; rheumatoid arthritis; lupus;								
KW	inflammatory bowel disease; multiple sclerosis; HIV; AIDS.								
XX									
OS	Homo sapiens.								
PN	WO2004042346-A2.								
XX									
XX	21-MAY-2004.								
XX	24-APR-2003; 2003WO-US012946.								
XX	24-APR-2002; 2002US-00131831.								
PR	20-DEC-2002; 2002US-00325899.								
XX	(EXPR-) EXPRESSION DIAGNOSTICS INC.								
PA	Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;								
PI	PI Rosenberg S;								
PI	DR 2004-400724/37.								
XX	Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
PT	PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
PT	PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
XX	Claim 65; SEQ ID NO 2509; 1762pp; English.								
XX	The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprising detecting the expression level of one or more genes. The methods and kits are useful in diagnosing or monitoring								
CC	CC	CC	CC	CC	CC	CC	CC	CC	XX
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
PS	PS 29-SEP-2003; 2003WO-US028547.								
XX	XX 02-OCT-2002; 2002US-0414971P.								
PD	PD 15-APR-2004.								
XX	XX 02004042346-A2.								
AC	AC ABM80784;								
XX	XX DT 18-NOV-2004 (first entry)								
DB	DB Tumour-associated antigenic target (TAT) polypeptide PRO81414, SEQ:2018.								
XX	XX Tumour-associated antigenic target; TAT; human; overexpression; cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytosstatic.								
XX	XX Homo sapiens.								
XX	XX OS WO2004042346-A2.								
XX	XX 21-MAY-2004.								
XX	XX 24-APR-2003; 2003WO-US012946.								
XX	XX 24-APR-2002; 2002US-00131831.								
PR	PR 20-DEC-2002; 2002US-00325899.								
XX	XX (EXPR-) EXPRESSION DIAGNOSTICS INC.								
PA	PA Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;								
PI	PI Rosenberg S;								
PI	PI DR 2004-400724/37.								
XX	XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
PT	PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
PT	PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
XX	XX Claim 65; SEQ ID NO 2509; 1762pp; English.								
XX	XX The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprising detecting the expression level of one or more genes. The methods and kits are useful in diagnosing or monitoring								
CC	CC	CC	CC	CC	CC	CC	CC	CC	XX
XX	XX 02004042346-A2.								
PD	PD 15-APR-2004.								
XX	XX 02004042346-A2.								
AC	AC ABM80784;								
XX	XX DT 18-NOV-2004 (first entry)								
DB	DB Tumour-associated antigenic target (TAT) polypeptide PRO81414, SEQ:2018.								
XX	XX Tumour-associated antigenic target; TAT; human; overexpression; cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytosstatic.								
XX	XX Homo sapiens.								
XX	XX OS WO2004042346-A2.								
XX	XX 21-MAY-2004.								
XX	XX 24-APR-2003; 2003WO-US012946.								
XX	XX 24-APR-2002; 2002US-00131831.								
PR	PR 20-DEC-2002; 2002US-00325899.								
XX	XX (EXPR-) EXPRESSION DIAGNOSTICS INC.								
PA	PA Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;								
PI	PI Rosenberg S;								
PI	PI DR 2004-400724/37.								
XX	XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
PT	PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
PT	PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
XX	XX Claim 65; SEQ ID NO 2509; 1762pp; English.								
XX	XX The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprising detecting the expression level of one or more genes. The methods and kits are useful in diagnosing or monitoring								
CC	CC	CC	CC	CC	CC	CC	CC	CC	XX
XX	XX 02004042346-A2.								
PD	PD 15-APR-2004.								
XX	XX 02004042346-A2.								
AC	AC ABM80784;								
XX	XX DT 18-NOV-2004 (first entry)								
DB	DB Tumour-associated antigenic target (TAT) polypeptide PRO81414, SEQ:2018.								
XX	XX Tumour-associated antigenic target; TAT; human; overexpression; cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytosstatic.								
XX	XX Homo sapiens.								
XX	XX OS WO2004042346-A2.								
XX	XX 21-MAY-2004.								
XX	XX 24-APR-2003; 2003WO-US012946.								
XX	XX 24-APR-2002; 2002US-00131831.								
PR	PR 20-DEC-2002; 2002US-00325899.								
XX	XX (EXPR-) EXPRESSION DIAGNOSTICS INC.								
PA	PA Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;								
PI	PI Rosenberg S;								
PI	PI DR 2004-400724/37.								
XX	XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
PT	PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
PT	PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
XX	XX Claim 65; SEQ ID NO 2509; 1762pp; English.								
XX	XX The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprising detecting the expression level of one or more genes. The methods and kits are useful in diagnosing or monitoring								
CC	CC	CC	CC	CC	CC	CC	CC	CC	XX
XX	XX 02004042346-A2.								
PD	PD 15-APR-2004.								
XX	XX 02004042346-A2.								
AC	AC ABM80784;								
XX	XX DT 18-NOV-2004 (first entry)								
DB	DB Tumour-associated antigenic target (TAT) polypeptide PRO81414, SEQ:2018.								
XX	XX Tumour-associated antigenic target; TAT; human; overexpression; cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytosstatic.								
XX	XX Homo sapiens.								
XX	XX OS WO2004042346-A2.								
XX	XX 21-MAY-2004.								
XX	XX 24-APR-2003; 2003WO-US012946.								
XX	XX 24-APR-2002; 2002US-00131831.								
PR	PR 20-DEC-2002; 2002US-00325899.								
XX	XX (EXPR-) EXPRESSION DIAGNOSTICS INC.								
PA	PA Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;								
PI	PI Rosenberg S;								
PI	PI DR 2004-400724/37.								
XX	XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
PT	PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
PT	PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
XX	XX Claim 65; SEQ ID NO 2509; 1762pp; English.								
XX	XX The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprising detecting the expression level of one or more genes. The methods and kits are useful in diagnosing or monitoring								
CC	CC	CC	CC	CC	CC	CC	CC	CC	XX
XX	XX 02004042346-A2.								
PD	PD 15-APR-2004.								
XX	XX 02004042346-A2.								
AC	AC ABM80784;								
XX	XX DT 18-NOV-2004 (first entry)								
DB	DB Tumour-associated antigenic target (TAT) polypeptide PRO81414, SEQ:2018.								
XX	XX Tumour-associated antigenic target; TAT; human; overexpression; cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytosstatic.								
XX	XX Homo sapiens.								
XX	XX OS WO2004042346-A2.								
XX	XX 21-MAY-2004.								
XX	XX 24-APR-2003; 2003WO-US012946.								
XX	XX 24-APR-2002; 2002US-00131831.								
PR	PR 20-DEC-2002; 2002US-00325899.								
XX	XX (EXPR-) EXPRESSION DIAGNOSTICS INC.								
PA	PA Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;								
PI	PI Rosenberg S;								
PI	PI DR 2004-400724/37.								
XX	XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
PT	PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
PT	PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.								
XX	XX Claim 65; SEQ ID NO 2509; 1762pp; English.								
XX	XX The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprising detecting the expression level of one or more genes. The methods and kits are useful in diagnosing or monitoring								
CC	CC	CC	CC	CC	CC	CC	CC	CC	XX
XX	XX 02004042346-A2.								
PD	PD 15-APR-2004.								
XX	XX 02004042346-A2.								
AC	AC ABM80784;								
XX	XX DT 18-NOV-2004 (first entry)								
DB	DB Tumour-associated antigenic target (TAT) polypeptide PRO81414, SEQ:2018.								
XX	XX Tumour-associated antigenic target; TAT; human; overexpression; cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytosstatic.								
XX	XX Homo sapiens.								
XX	XX OS WO2004042346-A2.								
XX	XX 21-MAY-2004.								
XX	XX 24-APR-2003; 2003WO-US012946.								
XX</td									

PA (GETH ) GENENTECH INC.  
 XX  
 PI Wu TD, Zhang Z, Zhou Y;  
 XX  
 DR WPI: 2004-347921/32.  
 DR N-PSDB; ACN38477.  
 XX  
 New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.

XX  
 PS Claim 12; SEQ ID NO 2018; 7273pp; English.  
 XX  
 CC The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to the TAT nucleic acids and polypeptides, expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention

XX  
 SQ Sequence 362 AA;

Query Match	72.1%	Score 261;	DB 8;	Length 362;
Best Local Similarity	99.7%	Pred. No. 1.4e-229;		
Matches 361;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy 1 MAPRSILLISGALALTDTWAGSHSLRYSTAVSRPGRGPYRIVAYEYDQPLRFSD 60  
 Db 1 MAPRSILLISGALALTDTWAGSHSLRYSTAVSRPGRGPYRIVAYEYDQPLRFSD 60

Qy 61 AAIPMPEPREPWVEQPGPOWENWTGYAKANAQTDVRLNLRYNNQEBAGSTLQRMN 120  
 Db 61 AAIPMPEPREPWVEQPGQIOWENWTGYAKANAQTDVRLNLRYNNQEBAGSTLQRMN 120

Qy 121 GCDMGPDGLRQYHQADGKDYISLNEDLSMTAQTDRYEAEEYAEFRTY 180  
 Db 121 GCDMGPDGLRQYHQADGKDYISLNEDLSMTAQTDRYEAEEYAEFRTY 180

Qy 181 LEGECLLELLRYYLENGLETIQLRADPKAHVAAHPPSDHEATLRCWALGYPAAETLTWQR 240  
 Db 181 LEGECLLELLRYYLENGLETIQLRADPKAHVAAHPPSDHEATLRCWALGYPAAETLTWQR 240

Qy 241 DGEBOEQDTDELVTRPAGDFTQKWAAYVPSGEGQRITCHVQHGLPQLTRWEQPQ 300  
 Db 241 DGEBOEQDTDELVTRPAGDFTQKWAAYVPSGEGQRITCHVQHGLPQLTRWEQSQ 300

Qy 301 PTIPIVGIVAGLVVGLVGAATGAVVAAVMRKSSDRNRGSYSQAATVDSAQGSEVSLTAN 360  
 Db 301 PTIPIVGIVAGLVVGLVGAATGAVVAAVMRKSSDRNRGSYSQAATVDSAQGSEVSLTAN 360

Qy 361 KV 362  
 Db 361 KV 362

XX  
 AC ADP23768;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 PRO polypeptide SEQ ID NO:946.

XX  
 KW PRO; antiinflammatory; antiarthritic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoratic; gene therapy; immune system.  
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.  
 XX  
 Unidentified.  
 OS  
 PN WO004041170-A2.  
 XX  
 PD 21-MAY-2004.  
 XX  
 PP 30-OCT-2003; 2003WO-US34312.  
 XX  
 PR 01-NOV-2002; 2002US-0423394P.

XX  
 (GETH ) GENENTECH INC.  
 XX  
 Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;  
 PI Wu TD;  
 XX  
 WPI; 2004-419628/39.  
 DR N-PSDB; ADP23767.

XX  
 PT New PRO polypeptides and polynucleotides, useful for treating e.g. erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system.  
 PT  
 PT  
 PT  
 PT  
 XX  
 PS Claim 7; SEQ ID NO 946; 2940pp; English.

XX  
 CC The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipsoratic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyrociditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infarction or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, Gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence represents a PRO protein of the invention.

XX  
 SQ Sequence 362 AA;

Query Match	72.1%	Score 261;	DB 8;	Length 362;
Best Local Similarity	99.7%	Pred. No. 1.4e-229;		
Matches 361;	Conservative 0;	Mismatches 1;	Indels 1;	Gaps 0;

Qy 1 MAPSILLISGALALTDTWAGSHSLRYSTAVSRPGRGPYRIVAYEYDQPLRFSD 60

Db 1 MAPSILLISGALALTDTWAGSHSLRYSTAVSRPGRGPYRIVAYEYDQPLRFSD 60

Qy 121 GCDMGPDGLRQYHQADGKDYISLNEDLSMTAQTDRYEAEEYAEFRTY 180

Db 121 GCDMGPDGLRQYHQADGKDYISLNEDLSMTAQTDRYEAEEYAEFRTY 180

Qy 181 LEGECLLELLRYYLENGLETIQLRADPKAHVAAHPPSDHEATLRCWALGYPAAETLTWQR 240

Db 181 LEGECLLELLRYYLENGLETIQLRADPKAHVAAHPPSDHEATLRCWALGYPAAETLTWQR 240

Qy 241 DGEBOEQDTDELVTRPAGDFTQKWAAYVPSGEGQRITCHVQHGLPQLTRWEQPQ 300

Db 241 DGEBOEQDTDELVTRPAGDFTQKWAAYVPSGEGQRITCHVQHGLPQLTRWEQSQ 300

Qy 301 PTIPIVGIVAGLVVGLVGAATGAVVAAVMRKSSDRNRGSYSQAATVDSAQGSEVSLTAN 360

Db 301 PTIPIVGIVAGLVVGLVGAATGAVVAAVMRKSSDRNRGSYSQAATVDSAQGSEVSLTAN 360

Qy 361 KV 362  
 Db 361 KV 362

XX  
 Score 261; DB 8; Length 362;  
 Best Local Similarity 99.7%; Pred. No. 1.4e-229;  
 Matches 361; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 MAPSILLISGALALTDTWAGSHSLRYSTAVSRPGRGPYRIVAYEYDQPLRFSD 60

Db 1 MAPSILLISGALALTDTWAGSHSLRYSTAVSRPGRGPYRIVAYEYDQPLRFSD 60

Qy	61 AAI PRME DREP PWY QEG QY WET TGYAKA NQ TDYVAL NLL RRYN QSEAG SHTLQGMN 120	FT Modified-site FT FT	331. .334 /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
Db	61 AAI PRME DREP PWY QEG QY WET TGYAKA NQ TDYVAL NLL RRYN QSEAG SHTLQGMN 120	FT Modified-site FT FT	352. .357 /note= "N-myristoylation site"
Qy	121 GCD MGDP DRLL RRG YH QHAYD GKD YISUN EDLS RSWTAADTVA QIT QTRFYEA EYAE FRTY 180	FT Modified-site FT FT	354. .359 /note= "N-myristoylation site"
Db	121 GCD MGDP DRLL RRG YH QHAYD GKD YISUN EDLS RSWTAADTVA QIT QTRFYEA EYAE FRTY 180	FT Region FT FT	360. .362 /note= "Microbodies C-terminal targeting signal"
Qy	181 LGE CCL KLL RRYL E N G L T L Q R D P K A K H V A H H P I S D H E A T L R C W A L G F Y P A E I T L T W Q R 240	XX XX	W02004081199-A2.
Db	181 LGE CCL KLL RRYL E N G L T L Q R D P K A K H V A H H P I S D H E A T L R C W A L G F Y P A E I T L T W Q R 240	PD 23 - SEP - 2004.	
Qy	241 D G B Q T Q T E L V E T R P A D G T F Q K W A V V V P S C E Q B Y T C H Y Q H E G L P Q P L I L R W Q S P Q 300	XX XX	PP 10 - MAR - 2004; 2004 WO - US007862.
Db	241 D G B Q T Q T E L V E T R P A D G T F Q K W A V V V P S C E Q B Y T C H Y Q H E G L P Q P L I L R W Q S P Q 300	XX XX	PR 11 - MAR - 2003; 2003 US - 0454025P.
Qy	301 P T I P V G I V A G L V V L G A V V T G A V V A A M W R K G S D R R G S Y S Q O A V T D S A Q Q S G V S L T A N 360	XX XX	(GETH ) GENENTECH INC.
Db	301 P T I P V G I V A G L V V L G A V V T G A V V A A M W R K G S D R R G S Y S Q O A V T D S A Q Q S G V S L T A N 360	PA PA	
Qy	361 KV 362	PI PI	Baldwin D, Bodary S, Clark H, Fong S, Gurney AL, Williams PM;
Db	361 KV 362	XX XX	WPI; 2004 - 668955 / 65.
RESULT 8	ADS74309 standard; protein; 362 AA.	PT PT	New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating psoriasis, Crohn's disease, Ulcerative colitis, or rheumatoid arthritis.
ADS74309		PT PT	Claim 9; SEQ ID NO 28; 160pp; English.
ID	ADS74309	PS PS	XX XX
AC	ADS74309;	XX XX	The present sequence is the protein sequence of novel human PRO polypeptide PRO8141. The invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to as PRO polypeptides that are useful in the diagnosis and treatment of immune-related diseases. Microarray analysis showed that expression of PRO8141 is up-regulated 1.2-fold in lesional skin as compared to non-lesional skin from psoriasis patients and up-regulated 1.5-fold in colon samples from ulcerative colitis patients as compared to normal colon. It is also down-regulated 2-fold upon differentiation of monocytes into macrophages after 7 days in differentiation media and up-regulated 4-fold in dendritic cells upon activation with LPS. PRO8141 can be used in a claimed method of identifying a compound that inhibits expression of the gene encoding it. The candidate compound is especially an antisense nucleic acid. The PRO polypeptide can be obtained by recombinant expression, especially in CHO, Escherichia coli or yeast host cells. The polypeptide, its antagonist or an antibody that binds the polypeptide are used in claimed methods for the alleviation or diagnosis of psoriasis and ulcerative colitis.
XX		XX XX	Sequence 362 AA;
XX		XX XX	Query Match 72.1%; Score 261; DB 8; Length 362;
XX		XX XX	Best Local Similarity 99.7%; Pred. No. 1.4e-229; Mismatches 361; Conservative 0; Indels 0; Gaps 0;
XX		XX XX	Matches 1 MAPRS ILLI S I S A L T D T W A G S H S L R Y F S A V S R D G R G P R Y A V E Y D D Q F Q L R F D S D 60
XX		XX XX	1 MAPRS ILLI S I S A L T D T W A G S H S L R Y F S A V S R D G R G P R Y A V E Y D D Q F Q L R F D S D 60
XX		XX XX	Qy 1 A A I P R E P R E P M V Q E P Q Y W E T G Y A K A N A Q T D Y V A L N I L R R Y N Q S E A G S H T L Q G M N 120
XX		XX XX	61 A A I P R E P R E P M V Q E P Q Y W E T G Y A K A N A Q T D Y V A L N I L R R Y N Q S E A G S H T L Q G M N 120
XX		XX XX	61 A A I P R E P R E P M V Q E P Q Y W E T G Y A K A N A Q T D Y V A L N I L R R Y N Q S E A G S H T L Q G M N 120
XX		XX XX	Qy 121 GCD MGDP DRLL RRG YH QHAYD GKD YISUN EDLS RSWTAADTVA QIT QTRFYEA EYAE FRTY 180
XX		XX XX	121 GCD MGDP DRLL RRG YH QHAYD GKD YISUN EDLS RSWTAADTVA QIT QTRFYEA EYAE FRTY 180
XX		XX XX	Db 121 GCD MGDP DRLL RRG YH QHAYD GKD YISUN EDLS RSWTAADTVA QIT QTRFYEA EYAE FRTY 180
XX		XX XX	181 L E G E C T E L L R R Y L E N G L T L Q R D P K A K H V A H H P I S D H E A T L R C W A L G F Y P A E I T L T W Q R 240
XX		XX XX	181 L E G E C T E L L R R Y L E N G L T L Q R D P K A K H V A H H P I S D H E A T L R C W A L G F Y P A E I T L T W Q R 240
XX		XX XX	241 D G B E Q T Q T E L V E T R P A D G T F Q K W A V V V P S C E Q B Y T C H Y Q H E G L P Q P L I L R W Q S P Q 300

			SQ Sequence 442 AA;
			Query Match 67.4%; Score 244; DB 7; Length 442;
			Best Local Similarity 95.7%; Pred. No. 5.7-214;
			Matches 344; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
		QY 1 MAPRSLLLISGALALTDTWAGSHSLRSTAVSRPGRGEPRYIAVEYVDDTQLRFDSQ 60	
		Db 1 MAPRSLLLISGALALTDTWAGSHSLRSTAVSRPGRGEPRYIAVEYVDDTQLRFDSQ 60	
		QY 61 AAIPRMEPREPVWEQGPQWENTGYAKANAOTDVALRNLRYNQSEAGSHTLQGMN 120	
		Db 61 AAIPRMEPREPVWEQGPQWENTGYAKANAOTDVALRNLRYNQSEAGSHTLQGMN 120	
		QY 121 GCDNGPDGRLLRGTHQAYDGKDYISLNEDLRSWTAADTVQQTQRFYEAEEFRTY 180	
		Db 121 GCDNGPDGRLLRGTHQAYDGKDYISLNEDLRSWTAADTVQQTQRFYEAEEFRTY 180	
		QY 181 LEGGCLELLRRLYRLENGLETQLRAPPKAHVAHHFISDHEATLRWALGYPAAETLTWQ 240	
		Db 181 LEGGCLELLRRLYRLENGLETQLRAPPKAHVAHHFISDHEATLRWALGYPAAETLTWQ 240	
		QY 241 DGEBOQTDLVTRPAGDGTFOWMQAAYVPSGEQEQRYTCHVQEGLPOLPLRWBOSQ 300	
		Db 241 DGEBOQTDLVTRPAGDGTFOWMQAAYVPSGEQEQRYTCHVQEGLPOLPLRWBOSQ 300	
		QY 301 PTIPIVGIVAGLVLTGAVTYAAMWRKSSDRNGSYSQA 345	
		Db 301 PTIPIVGIVAGLVLTGAVTYAAMWRKSSDRNGSYSQA 345	
		RESULT 1.0	
		ID AAB43986 Standard; protein; 271 AA.	
		XX	
		AC AAB43986;	
		XX	
		DT 08-FEB-2001 (first entry)	
		XX	
		Human cancer associated protein sequence SEQ ID NO:1431.	
		DE XX	
		KW Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytosolic; proliferative; vunlarer; immunomodulator;	
		KW antidiabetic; antiasthmatic; antirheumatic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; hematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.	
		KW Homo sapiens.	
		XX	
		PN WO2003087768-A2.	
		XX	
		PD 23-OCT-2003.	
		XX	
		PF 04-APR-2003; 2003WO-US010870.	
		XX	
		PR 12-APR-2002; 2002US-0372843P.	
		PR 17-JUN-2002; 2002US-038987P.	
		PR 20-SEP-2002; 2002US-0412418P.	
		XX	
		(MTO-) MITOKOR.	
		PA (BUCK) BUCK INST AGE RES.	
		XX	
		PJ Ghosh SS, Fany ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;	
		PI Warnock DE;	
		XX	
		DR WPI; 2003-845369/78.	
		XX	
		PT Identifying a mitochondrial target for drug screening assays and for	
		PT treating diseases associated with altered mitochondrial function,	
		PT comprises detecting a modified polypeptide in a sample and correlating	
		PT with the disease.	
		XX	
		PS Claim 1; SEQ ID NO 1887; 180pp; English.	
		XX	
		CC This invention relates to novel mitochondrial targets that can be used	
		CC for therapeutic intervention in treating a disease associated with	
		CC altered mitochondrial function. Specifically, it refers to a method for	
		CC identifying proteins of the human heart mitochondrial proteome that are	
		CC useful for drug screening assays, as well as therapeutic targets. The	
		CC present invention describes a method for identifying such proteins that	
		CC can be used in the treatment of various diseases associated with altered	
		CC mitochondrial function including diabetes mellitus, Huntington's disease,	
		CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial	
		CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy	
		CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these	
		CC compositions have neuroprotective, nootropic, antidiabetic,	
		CC cytoprotective, antiarthritic, osteopathic, ophthalmological and	
		CC mitochondrial protein of the invention.	
		XX	
		CC Novel isolated nucleic acids comprising sequences encoding peptides	
		CC useful for treating or diagnosing e.g. cancer.	
		XX	
		PS Claim 11; Page 2115-2116; 2352pp; English.	

XX AAC77607 to AAC78448 encode the human cancer associated proteins given in  
 CC AAB4338 to AAB4239. The Proteins can have activities based on the  
 CC tissues and cells. The genes are expressed in. Example of activities  
 CC include: cytosolic; proliferative; pulmonary; immunomodulator;  
 CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;  
 CC antiinflammatory; thyroid; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiotonic; thrombolytic;  
 CC coagulant;  
 CC nootropic; vasoactive; antipsoriatic and antiangiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic disease, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
 CC AAC78457 and AAB4240 represent sequences used in the exemplification of  
 CC the present invention  
 XX Sequence 271 AA;

Query Match 54.1%; Score 196; DB 3; Length 271;

Best Local Similarity 100.0%; Pred. No. 2.6e-170; Mismatches 0; Indels 0; Gaps 0;

Matches 1.9e-170; Conservative 0; Gaps 0; Gaps 0;

Db 1 MAPRSLLLSSGALATTWAGSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFSD 60

Qy 7 MAPRSLLLSSGALATTWAGSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFSD 66

Db 61 AAIPRMERPREPWEQEGPYWETTGAKANAQTDRVALNLLRRYNQSEAGSHTLQGMN 120

Qy 67 AAIPRMERPREPWEQEGPYWETTGAKANAQTDRVALNLLRRYNQSEAGSHTLQGMN 126

Db 121 GCDMGPGPRLLACYHOMYDGKDYISNEDLRSWTAAITVAQITQTYEARAYAEEFRY 180

Qy 127 GCDMGPGPRLLACYHOMYDGKDYISNEDLRSWTAAITVAQITQTYEARAYAEEFRY 186

Db 181 LEGCCLLELLRRLYLENG 196

Qy 187 LEGCCLLELLRRLYLENG 202

Db 370 AAIPRMERPREPWEQEGPYWETTGAKANAQTDRVALNLLRRYNQSEAGSHTLQGMN 120

Qy 310 MAPRSLLLSSGALATTWAGSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFSD 369

Db 61 AAIPRMERPREPWEQEGPYWETTGAKANAQTDRVALNLLRRYNQSEAGSHTLQGMN 120

Qy 370 AAIPRMERPREPWEQEGPYWETTGAKANAQTDRVALNLLRRYNQSEAGSHTLQGMN 429

Db 121 GCDMGPGPRLLACYHOMYDGKDYISNEDLRSWTAAITVAQITQTYEARAYAEEFRY 180

Qy 430 GCDMGPGPRLLACYHOMYDGKDYISNEDLRSWTAAITVAQITQTYEARAYAEEFRY 489

Db 490 LEGCCLLELLRRLYLENG 505

RESULT 12  
 AAG64518

ID AAG64518 standard; protein; 274 AA.

XX AC AAG64518;

XX DT 12-SEP-2001 (first entry)

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX AC AAG64518;

XX XX Human cancer cell specific HLA-F antigen SEQ ID 5.

XX OS XX Human cancer cell specific HLA-F antigen; protein; 274 AA.

XX 30-SEP-1999; 99JP-00279566.  
 PF 30-SEP-1999; 99JP-00279566.  
 XX  
 PR (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA K.  
 XX DR WPI; 2001-360493/38.  
 XX N-PSDB; AAH45556.  
 Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
 XX  
 PS Claim 2; Page 10-11; 12BP; Japanese.  
 CC This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the invention.  
 XX Sequence 274 AA;  
 SQ Query Match 48.3%; Score 175; DB 4; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-151;  
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 22 GSHSLRYFSTAVSRPGRGEPRTYAVEYDDTQFLRFDSDAAIPRMEEPRPWVEQGPQYW 81  
 Db 1 GSHSLRYFSTAVSRPGRGEPRTYAVEYDDTQFLRFDSDAAIPRMEEPRPWVEQGPQYW 60  
 Qy 82 EWTGYAKANAQTDRVALNLRLRYNQSSEAGSHTLQGRNGCDMGPDGRILLRGYHQAYDG 141  
 Db 61 EWTGYAKANAQTDRVALNLRLRYNQSSEAGSHTLQGRNGCDMGPDGRILLRGYHQAYDG 120  
 Qy 142 KDYISLNEDLRSWTAADTVQITQRFYAEYEAEFRTYLEGCELLRRYLENG 196  
 Db 61 EWTGYAKANAQTDRVALNLRLRYNQSSEAGSHTLQGRNGCDMGPDGRILLRGYHQAYDG 175  
 Qy 142 KDYISLNEDLRSWTAADTVQITQRFYAEYEAEFRTYLEGCELLRRYLENG 196  
 Db 121 KDYISLNEDLRSWTAADTVQITQRFYAEYEAEFRTYLEGCELLRRYLENG 175  
 RESULT 14  
 ID AAC64619 standard; protein: 215 AA.  
 XX  
 AC AAC64619;  
 XX DT 12-SEP-2001 (first entry)  
 ID AAC64619;  
 XX DE Human cancer cell specific HLA-F antigen SEQ ID 6.  
 XX KW HLA-F antigen; cancer cell specific; human.  
 OS Homo sapiens.  
 XX PR 30-SEP-1999; 99JP-00279566.  
 XX PN JP2001095584-A.  
 AC ADP55588 standard; protein: 274 AA.  
 XX  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 13  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 12  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 11  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 10  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 9  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 8  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 7  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 6  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 5  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 4  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 3  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 2  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.  
 RESULT 1  
 ID ADP55588  
 XX ADP55588 standard; protein: 274 AA.  
 AC ADP55588;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX OS Homo sapiens.  
 XX PN JP200312544-A.  
 XX PD 15-JAN-2003.  
 XX PP 27-MAR-2002; 2002JP-00088991.  
 XX PR 27-MAR-2001; 2001JP-00090121.  
 PA (EGAW/ ) EGAWA K.  
 PA (MEDI- ) MEDINET KK.  
 PA (KIMU/ ) KIMURA Y.  
 XX DR WPI; 2003-486263/46.  
 XX N-PSDB; ADF55588.

CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
 CC used in a method to diagnose cancer, in which the protein is used to  
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
 CC invention represents the cancer cell-specific HLA-F antigen of the  
 CC invention.

XX Sequence 215 AA;

Query Match 42.3%; Score 153; DB 4; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-131;  
 Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SQ Sequence 215 AA;

```

Qy 4 IAVEYVDDTQFLRFDSDAAIPRMPEPREPWWQECPQYEWNTGYAKANAAQTDRVALRNLL 103
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 IAVEYVDDTQFLRFDSDAAIPRMPEPREPWWQECPQYEWNTGYAKANAAQTDRVALRNLL 60
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 104 RRYNQSEAGSHTLQGNGCDMGPDRLLRGTHQAYDGKDYLISNEPDLSWTAADTVQI 163
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 RRYNQSEAGSHTLQGNGCDMGPDRLLRGTHQAYDGKDYLISNEPDLSWTAADTVQI 120
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 164 TORFYEAEEYAAEERTYLEGECLELLRRYLENG 196
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 TORFYEAEEYAAEERTYLEGECLELLRRYLENG 153
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: July 13, 2005, 09:14:41  
 Job time : 168 secs

## RESULT 15

ID ADF55589 standard; protein; 215 AA.  
 XX

AC ADF55589;

XX DT 12-FEB-2004 (first entry)

XX DE Fragment #2 of human cancer-cell specific HLA-F antigen.

XX Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.

XX OS Homo sapiens.

XX PN JP2003012544-A.

XX PD 15-JAN-2003.

XX PP 27-MAR-2002; 2002JP-00088931.

XX PR 27-MAR-2001; 2001JP-00090121.

XX XX (EGAWA /) EGAWA K.

PA PA (MBDI -) MEDINET K.K.

PA (KIMU /) KIMURA Y.

XX DR WPI; 2003-486263/46.

DR N-PSDB; ADF55586.

XX PR Agent for preventing and treating cancer, comprising human leukocyte

PR antigen-F DNA, or a plasmid or viral vector comprising the DNA.

XX PS XX Claim 7; SEQ ID NO 6; 19pp. Japanese.

The present invention relates to an agent for preventing or treating cancer. The agent comprises a portion or a complete sequence of a human leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of presenting a cancer-cell specific antigen transformed with HLA-F DNA, or a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte (CTL) inducer which induces CTL which is non-specific to an organ, is unrestricted to the major histocompatibility complex (MHC) and specific to a cancer cell, and an anti-HLA-F antibody. The agent of the invention is useful for treating or preventing cancer. A cell capable of presenting a cancer-cell specific antigen is useful for measuring HLA-F antigen and for diagnosing cancer. The present sequence represents part of the human cancer-cell specific HLA-F antigen.